

Amelt C

1



SEQUENCE LISTING

<110> Wright, David A.
Voytas, Daniel F.

<120> PLANT RETROELEMENTS AND METHODS RELATED THERETO

<130> P-1065A

<140> 09/586,106

<141> 2000-06-02

<150> 60/087,125

<151> 1998-05-29

<150> 09/322,478

<151> 1999-05-28

<160> 190

<170> FastSEQ for Windows Version 4.0

<210> 1

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<212> DNA

<213> Glycine max

<400> 1

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18

<210> 2

<211> 18

<212> DNA

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<211> 6

<212> DNA

<213> Glycine max

<400> 3

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6

<210> 4

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 4

Met Ala Ser Arg Lys Arg Lys

1

5

<210> 5

<211> 1263

<212> DNA

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

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atccttccag	agaggaatgt	agagcttggg	ccagggatgt	ttgatgagtt	cctgcaggaa	180
ctccagaggc	tcagatggga	ccagggttctg	acccgacttc	cagagaagtg	gattgatgtt	240
gctctggtga	aggagtttta	ctccaaccta	tatgatccag	aggaccacag	tccgaagttt	300
tggaagtgtc	gaggacaggt	tgtgagattt	gatgctgaga	cgattaatga	tttctcgcac	360
accccggtca	tcttggcaga	gggagaggat	tatccagcct	actctcagta	cctcagcact	420
cctccagacc	atgatgccat	cctttccgct	ctgtgtactc	cagggggacg	atttgttctg	480
aatggtgata	gtgccccctg	gaagctgctg	cggaaggatc	tgatgacgct	cgcgagaca	540
tggaagtgtc	tctcttattt	taaccttgca	ctgacttttc	acacttctga	tattaatgtt	600
gacagggccc	gactcaatta	tggttggtg	atgaagatgg	acctggacgt	gggcagcctc	660
atctctcttc	agatcagtc	gatcgcccag	tccatcactt	ccaggcttgg	gttcccagcg	720
ttgatcacia	cactgtgtga	gattcagggg	gttgctctctg	ataccctgat	ttttgagtca	780
ctcagtcctg	tgatcaacct	tgcttacatt	aagaagaact	gctggaaccc	tgccgatcca	840
tctatcacat	ttcagggggac	cgccgcacg	cgcaccagag	cttcggcgctc	ggcatctgag	900
gctcctcttc	catcccagca	tccttctcag	cctttttccc	agagaccacg	gcctccactt	960
ctatccacct	cagcacctcc	atacatgcat	ggacagatgc	tcaggtcctt	gtaccagggg	1020
cagcagatca	tcattcagaa	cctgtatcga	ttgtccctac	atttgagat	ggatctgcca	1080
ctcatgactc	cggaggccta	tcgtcagcag	gtcgccaagc	taggagacca	gccctccact	1140
gacagggggg	aagagccttc	tggaagccgt	gctactgagg	atcctgccgt	tgatgaagac	1200
ctcatagctg	acttggtctg	cgctgattgg	agcccatggg	cagacttggg	cagaggcagc	1260
tga						1263

<210> 6

<211> 421

<212> PRT

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 6

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Asn	Trp	Asp	Ser	Ser	Arg	Phe	Thr	Phe	Glu	Ile	Ala	Trp	His	Arg	Tyr
			20					25					30		
Gln	Asp	Ser	Ile	Gln	Leu	Arg	Asn	Ile	Leu	Pro	Glu	Arg	Asn	Val	Glu
		35				40						45			
Leu	Gly	Pro	Gly	Met	Phe	Asp	Glu	Phe	Leu	Gln	Glu	Leu	Gln	Arg	Leu
	50				55				60						
Arg	Trp	Asp	Gln	Val	Leu	Thr	Arg	Leu	Pro	Glu	Lys	Trp	Ile	Asp	Val
65				70				75						80	
Ala	Leu	Val	Lys	Glu	Phe	Tyr	Ser	Asn	Leu	Tyr	Asp	Pro	Glu	Asp	His
			85				90						95		
Ser	Pro	Lys	Phe	Trp	Ser	Val	Arg	Gly	Gln	Val	Val	Arg	Phe	Asp	Ala
		100					105						110		

Glu Thr Ile Asn Asp Phe Leu Asp Thr Pro Val Ile Leu Ala Glu Gly
 115 120 125
 Glu Asp Tyr Pro Ala Tyr Ser Gln Tyr Leu Ser Thr Pro Pro Asp His
 130 135 140
 Asp Ala Ile Leu Ser Ala Leu Cys Thr Pro Gly Gly Arg Phe Val Leu
 145 150 155 160
 Asn Val Asp Ser Ala Pro Trp Lys Leu Leu Arg Lys Asp Leu Met Thr
 165 170 175
 Leu Ala Gln Thr Trp Ser Val Leu Ser Tyr Phe Asn Leu Ala Leu Thr
 180 185 190
 Phe His Thr Ser Asp Ile Asn Val Asp Arg Ala Arg Leu Asn Tyr Gly
 195 200 205
 Leu Val Met Lys Met Asp Leu Asp Val Gly Ser Leu Ile Ser Leu Gln
 210 215 220
 Ile Ser Gln Ile Ala Gln Ser Ile Thr Ser Arg Leu Gly Phe Pro Ala
 225 230 235 240
 Leu Ile Thr Thr Leu Cys Glu Ile Gln Gly Val Val Ser Asp Thr Leu
 245 250 255
 Ile Phe Glu Ser Leu Ser Pro Val Ile Asn Leu Ala Tyr Ile Lys Lys
 260 265 270
 Asn Cys Trp Asn Pro Ala Asp Pro Ser Ile Thr Phe Gln Gly Thr Arg
 275 280 285
 Arg Thr Arg Thr Arg Ala Ser Ala Ser Ala Ser Glu Ala Pro Leu Pro
 290 295 300
 Ser Gln His Pro Ser Gln Pro Phe Ser Gln Arg Pro Arg Pro Pro Leu
 305 310 315 320
 Leu Ser Thr Ser Ala Pro Pro Tyr Met His Gly Gln Met Leu Arg Ser
 325 330 335
 Leu Tyr Gln Gly Gln Gln Ile Ile Ile Gln Asn Leu Tyr Arg Leu Ser
 340 345 350
 Leu His Leu Gln Met Asp Leu Pro Leu Met Thr Pro Glu Ala Tyr Arg
 355 360 365
 Gln Gln Val Ala Lys Leu Gly Asp Gln Pro Ser Thr Asp Arg Gly Glu
 370 375 380
 Glu Pro Ser Gly Ala Ala Thr Glu Asp Pro Ala Val Asp Glu Asp
 385 390 395 400
 Leu Ile Ala Asp Leu Ala Gly Ala Asp Trp Ser Pro Trp Ala Asp Leu
 405 410 415
 Gly Arg Gly Ser Glx
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<210> 7

<211> 1596

<212> DNA

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 7

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tgctggcgta	acaacgctgc	aagaagaaga	agggagcaag	acatagaagg	aagtagttac	120
acctcacctc	ctccttctcc	aaattatgct	cagatggacg	gggaaccggc	acaaagagtc	180
acactagagg	acttctctaa	taccaccact	cctcagttct	ttacaagtat	cacaaggccg	240
gaagtccaag	cagatctcct	tactcaaggg	aacctcttcc	atggtcttcc	aaatgaagat	300
ccatatgcgc	atctagcctc	atacatagag	atatgcagca	ccgttaaaat	cgccggagtt	360
cctaaagatg	cgatactcct	taacctcttt	tccttttccc	tagcaggaga	ggcaaaaaga	420

tggttgact	cctttaagg	caatagctta	agaacatggg	aagaagtagt	ggaaaaattc	480
ttaaagaagt	atttcccaga	gtcaaagacc	gtcgaacgaa	agatggagat	ttcttatttc	540
catcaatttc	tggtatgaatc	ccttagcgaa	gcactagacc	atttccacgg	attgctaaga	600
aaaacaccaa	cacacagata	cagcgagcca	gtacaactaa	acatattcat	cgatgacttg	660
caactcttaa	tcgaaacagc	tactagaggg	aagatcaagc	tgaagactcc	cgaagaagcg	720
atggagctcg	tcgagaacat	ggcggctagc	gatcaagcaa	tccttcatga	tcacacttat	780
gttcccacaa	aaagaagcct	cttggagctt	agcacgcagg	acgcaacttt	ggtacaaaac	840
aagctgttga	cgaggcagat	agaagccctc	atcgaaaccc	tcagcaagct	gcctcaacaa	900
ttacaagcga	taagttcttc	ccactcttct	gttttgagg	tagaagaatg	ccccacatgc	960
agagggacac	atgagcctgg	acaatgtgca	agccaacaag	acccctctcg	tgaagtaa	1020
tatataggca	tactaaatcg	ttacggattt	cagggctaca	accagggaaa	tccatctgga	1080
ttcaatcaag	gggcaacaag	atttaatcac	gagccaccgg	ggtttaatca	aggaagaaac	1140
ttcatgcaag	gctcaagttg	gacgaataaa	ggaaatcaat	ataaggagca	aaggaaccaa	1200
ccaccatacc	agccaccata	ccagcaccct	agccaaggtc	cgaatcagca	agaaaagccc	1260
acaaaaatag	aggaactgct	gctgcaattc	atcaaggaga	caagatcaca	tcaaaaagagc	1320
acggatgcag	ccattcgga	tctagaagtt	caaattgggcc	aactggcgca	tgacaaagcc	1380
gaacggccca	ctagaacttt	cggtgctaac	atggagagaa	gaaccccaag	gaaggataaa	1440
gcagtactga	ctagagggga	gagaagagcg	caggagagag	gtaagggtga	aggagaagac	1500
tgccagaag	aaggaaggac	agagaagaca	gaagaagaag	agaagggtgc	agaagaacct	1560
aagcgtacca	agagccagag	agcaaggga	gccaag			1596

<210> 8

<211> 532

<212> PRT

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 8

Met	Arg	Gly	Arg	Thr	Ala	Ser	Gly	Asp	Val	Val	Pro	Ile	Asn	Leu	Glu
1				5				10						15	
Ile	Glu	Ala	Thr	Cys	Arg	Arg	Asn	Asn	Ala	Ala	Arg	Arg	Arg	Arg	Glu
			20					25					30		
Gln	Asp	Ile	Glu	Gly	Ser	Ser	Tyr	Thr	Ser	Pro	Pro	Pro	Ser	Pro	Asn
		35					40					45			
Tyr	Ala	Gln	Met	Asp	Gly	Glu	Pro	Ala	Gln	Arg	Val	Thr	Leu	Glu	Asp
	50					55				60					
Phe	Ser	Asn	Thr	Thr	Thr	Pro	Gln	Phe	Phe	Thr	Ser	Ile	Thr	Arg	Pro
65					70					75				80	
Glu	Val	Gln	Ala	Asp	Leu	Leu	Thr	Gln	Gly	Asn	Leu	Phe	His	Gly	Leu
				85					90					95	
Pro	Asn	Glu	Asp	Pro	Tyr	Ala	His	Leu	Ala	Ser	Tyr	Ile	Glu	Ile	Cys
		100						105					110		
Ser	Thr	Val	Lys	Ile	Ala	Gly	Val	Pro	Lys	Asp	Ala	Ile	Leu	Leu	Asn
	115						120					125			
Leu	Phe	Ser	Phe	Ser	Leu	Ala	Gly	Glu	Ala	Lys	Arg	Trp	Leu	His	Ser
	130					135					140				
Phe	Lys	Gly	Asn	Ser	Leu	Arg	Thr	Trp	Glu	Glu	Val	Val	Glu	Lys	Phe
145					150					155				160	
Leu	Lys	Lys	Tyr	Phe	Pro	Glu	Ser	Lys	Thr	Val	Glu	Arg	Lys	Met	Glu
			165						170					175	
Ile	Ser	Tyr	Phe	His	Gln	Phe	Leu	Asp	Glu	Ser	Leu	Ser	Glu	Ala	Leu
		180						185					190		
Asp	His	Phe	His	Gly	Leu	Leu	Arg	Lys	Thr	Pro	Thr	His	Arg	Tyr	Ser
	195						200					205			
Glu	Pro	Val	Gln	Leu	Asn	Ile	Phe	Ile	Asp	Asp	Leu	Gln	Leu	Leu	Ile

210		215		220
Glu Thr Ala Thr Arg	Gly Lys Ile Lys Leu	Lys Thr Pro Glu Glu Ala		
225	230	235		240
Met Glu Leu Val Glu	Asn Met Ala Ala Ser	Asp Gln Ala Ile Leu His		
	245	250		255
Asp His Thr Tyr Val	Pro Thr Lys Arg Ser	Leu Leu Glu Leu Ser Thr		
	260	265		270
Gln Asp Ala Thr Leu	Val Gln Asn Lys Leu	Leu Thr Arg Gln Ile Glu		
	275	280		285
Ala Leu Ile Glu Thr	Leu Ser Lys Leu Pro	Gln Gln Leu Gln Ala Ile		
	290	295		300
Ser Ser Ser His Ser	Ser Val Leu Gln Val	Glu Glu Cys Pro Thr Cys		
305	310	315		320
Arg Gly Thr His Glu	Pro Gly Gln Cys Ala	Ser Gln Gln Asp Pro Ser		
	325	330		335
Arg Glu Val Asn Tyr	Ile Gly Ile Leu Asn	Arg Tyr Gly Phe Gln Gly		
	340	345		350
Tyr Asn Gln Gly Asn	Pro Ser Gly Phe Asn	Gln Gly Ala Thr Arg Phe		
	355	360		365
Asn His Glu Pro Pro	Gly Phe Asn Gln Gly	Arg Asn Phe Met Gln Gly		
	370	375		380
Ser Ser Trp Thr Asn	Lys Gly Asn Gln Tyr	Lys Glu Gln Arg Asn Gln		
385	390	395		400
Pro Pro Tyr Gln Pro	Pro Tyr Gln His Pro	Ser Gln Gly Pro Asn Gln		
	405	410		415
Gln Glu Lys Pro Thr	Lys Ile Glu Glu Leu	Leu Leu Gln Phe Ile Lys		
	420	425		430
Glu Thr Arg Ser His	Gln Lys Ser Thr Asp	Ala Ala Ile Arg Asn Leu		
	435	440		445
Glu Val Gln Met Gly	Gln Leu Ala His Asp	Lys Ala Glu Arg Pro Thr		
	450	455		460
Arg Thr Phe Gly Ala	Asn Met Glu Arg Arg	Thr Pro Arg Lys Asp Lys		
465	470	475		480
Ala Val Leu Thr Arg	Gly Gln Arg Arg Ala	Gln Glu Glu Gly Lys Val		
	485	490		495
Glu Gly Glu Asp Trp	Pro Glu Glu Gly Arg	Thr Glu Lys Thr Glu Glu		
	500	505		510
Glu Glu Lys Val Ala	Glu Glu Pro Lys Arg	Thr Lys Ser Gln Arg Ala		
	515	520		525
Arg Glu Ala Lys				
530				

<210> 9

<211> 603

<212> DNA

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 9

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tcatacgga atgtctacat cttggtagct gtggattacg tctccaaatg ggtggaagcc	180
atagccacgc caaaggacga tgccagggtg gtgatcaaat ttctgaagaa gaacattttt	240
tcccgttttg gagtcccacg agccttgatt agtgataggg gaacgcactt ctgcaacaat	300
cagttgaaga aagtcttgga gcactataat gtccgacata aggtggccac accttatcac	360

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cctcagacaa atggccaagc agaaatttct aacagggagc tcaagcgaat cctggaaaag 420
acagttgcat caacaagaaa ggattggtcc ttgaagctcg atgatgctct ctgggcctat 480
aggacagcgt tcaagactcc catcggtta tcaccatttc agctagtgtg tgggaaggca 540
tgtcatttac cagtggagct ggagtacaaa gcatattggg ctctcaagtt gctcaacttt 600
gac 603

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<210> 10
 <211> 201
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> plant retroelement sequence

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<400> 10
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Pro Leu Gln Asn Ile Met Glu Val Glu Ile Phe Asp Cys Trp Gly Ile
20     25     30
Asp Phe Met Gly Pro Phe Pro Ser Tyr Gly Asn Val Tyr Ile Leu
35     40     45
Val Ala Val Asp Tyr Val Ser Lys Trp Val Glu Ala Ile Ala Thr Pro
50     55     60
Lys Asp Asp Ala Arg Val Val Ile Lys Phe Leu Lys Lys Asn Ile Phe
65     70     75     80
Ser Arg Phe Gly Val Pro Arg Ala Leu Ile Ser Asp Arg Gly Thr His
85     90     95
Phe Cys Asn Asn Gln Leu Lys Lys Val Leu Glu His Tyr Asn Val Arg
100    105    110
His Lys Val Ala Thr Pro Tyr His Pro Gln Thr Asn Gly Gln Ala Glu
115    120    125
Ile Ser Asn Arg Glu Leu Lys Arg Ile Leu Glu Lys Thr Val Ala Ser
130    135    140
Thr Arg Lys Asp Trp Ser Leu Lys Leu Asp Asp Ala Leu Trp Ala Tyr
145    150    155    160
Arg Thr Ala Phe Lys Thr Pro Ile Gly Leu Ser Pro Phe Gln Leu Val
165    170    175
Tyr Gly Lys Ala Cys His Leu Pro Val Glu Leu Glu Tyr Lys Ala Tyr
180    185    190
Trp Ala Leu Lys Leu Leu Asn Phe Asp
195    200

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<210> 11
 <211> 600
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> plant retroelement sequence

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<400> 11
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cgaactgtca ctggttggcg aatgtgtatc gactatcgca agctgaatga agccacacgg 180
aaggaccatt tccccttacc ttatcatggat cagatgctgg agagacttgc agggcaggca 240
tactactgtt tcttggatgg atactcggga tacaaccaga tcgcggtaga cccagagat 300
caggagaaga cggcctttac atgccccttt ggcgtctttg cttacagaag gatgccattc 360

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gggttatgta atgcaccagc cacatttcag aggtgcatgc tggccatttt ttcagacatg	420
gtggagaaaa gcatcgaggt atttatggac gacttctcgg tttttggacc ctcatattgac	480
agctgtttga ggaacctaga gaggtactt cagaggtgcg aagagactaa cttggtactg	540
aattgggaaa agtgtcattt catggttcga gagggcatag tcctaggcca caagatctca	600

<210> 12

<211> 200

<212> PRT

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 12

Leu	Glu	Ala	Gly	Leu	Ile	Tyr	Pro	Ile	Ser	Asp	Ser	Ala	Trp	Val	Ser
1			5						10					15	
Pro	Val	Gln	Val	Val	Pro	Lys	Lys	Gly	Met	Thr	Val	Val	Arg	Asp	
		20						25				30			
Glu	Arg	Asn	Asp	Leu	Ile	Pro	Thr	Arg	Thr	Val	Thr	Gly	Trp	Arg	Met
		35					40				45				
Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn	Glu	Ala	Thr	Arg	Lys	Asp	His	Phe
50						55				60					
Pro	Leu	Pro	Phe	Met	Asp	Gln	Met	Leu	Glu	Arg	Leu	Ala	Gly	Gln	Ala
65					70				75					80	
Tyr	Tyr	Cys	Phe	Leu	Asp	Gly	Tyr	Ser	Gly	Tyr	Asn	Gln	Ile	Ala	Val
			85					90					95		
Asp	Pro	Arg	Asp	Gln	Glu	Lys	Thr	Ala	Phe	Thr	Cys	Pro	Phe	Gly	Val
			100					105					110		
Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe	Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr
		115					120					125			
Phe	Gln	Arg	Cys	Met	Leu	Ala	Ile	Phe	Ser	Asp	Met	Val	Glu	Lys	Ser
130					135					140					
Ile	Glu	Val	Phe	Met	Asp	Asp	Phe	Ser	Val	Phe	Gly	Pro	Ser	Phe	Asp
145				150					155					160	
Ser	Cys	Leu	Arg	Asn	Leu	Glu	Arg	Val	Leu	Gln	Arg	Cys	Glu	Glu	Thr
			165					170					175		
Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys	Cys	His	Phe	Met	Val	Arg	Glu	Gly
		180					185						190		
Ile	Val	Leu	Gly	His	Lys	Ile	Ser								
		195					200								

<210> 13

<211> 858

<212> DNA

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 13

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ccattcgggg aagccttaca gcagatgccc ctctactcca aatttatgaa agacatcctc	180
accaagaagg ggaagtatat tgacaacgag aatattgtgg taggaggcaa ttgcagtgcg	240
ataatacaaa ggattctacc caagaagttt aaagaccccg gaagtgttac catcccgtgc	300
accattggga aggaagccgt aaacaaggcc ctcatgtatc taggagcaag tatcaatctg	360
atgcccttgt caatgtgcaa aagaattggg aatttgaaga tagatccac caagatgacg	420

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cttcaactgg cagaccgctc aatcacaagg ccatatgggg tggtagaaga tgtcctggtc 480
aagggtacgcc acttcacttt tccggtggac tttgttatca tggatatcga agaagacact 540
gagattcccc ttatcttagg cagacccttc atgctgactg ccaactgtgt ggtggatatg 600
gggaaagggg acttagagtt gactattgat aatcagaaga tcaccttga cttatcaag 660
gcaatgaagt acccacagga gggttggaag tgcttcagaa tagaggagat tgatgaggaa 720
gatgtcagtt ttctcgagac accaaagact tcgctagaaa aagcaatggt aaatcattta 780
gactgtctaa ccagtgaaga ggaagaagat ctgaaggctt gcttggaataa cttggatcaa 840
gaagacagta ttcctgag                                     858

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<210> 14

<211> 286

<212> PRT

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 14

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Lys Glu Glu Pro Leu Ala Leu Pro Gln Asp Leu Pro Tyr Pro Met Ala
1          5          10          15
Pro Thr Lys Lys Asn Lys Glu Arg Tyr Phe Ala Arg Phe Leu Glu Ile
20          25          30
Phe Lys Gly Leu Glu Ile Thr Met Pro Phe Gly Glu Ala Leu Gln Gln
35          40          45
Met Pro Leu Tyr Ser Lys Phe Met Lys Asp Ile Leu Thr Lys Lys Gly
50          55          60
Lys Tyr Ile Asp Asn Glu Asn Ile Val Val Gly Gly Asn Cys Ser Ala
65          70          75          80
Ile Ile Gln Arg Ile Leu Pro Lys Lys Phe Lys Asp Pro Gly Ser Val
85          90          95
Thr Ile Pro Cys Thr Ile Gly Lys Glu Ala Val Asn Lys Ala Leu Ile
100         105         110
Asp Leu Gly Ala Ser Ile Asn Leu Met Pro Leu Ser Met Cys Lys Arg
115         120         125
Ile Gly Asn Leu Lys Ile Asp Pro Thr Lys Met Thr Leu Gln Leu Ala
130         135         140
Asp Arg Ser Ile Thr Arg Pro Tyr Gly Val Val Glu Asp Val Leu Val
145         150         155         160
Lys Val Arg His Phe Thr Phe Pro Val Asp Phe Val Ile Met Asp Ile
165         170         175
Glu Glu Asp Thr Glu Ile Pro Leu Ile Leu Gly Arg Pro Phe Met Leu
180         185         190
Thr Ala Asn Cys Val Val Asp Met Gly Lys Gly Asn Leu Glu Leu Thr
195         200         205
Ile Asp Asn Gln Lys Ile Thr Phe Asp Leu Ile Lys Ala Met Lys Tyr
210         215         220
Pro Gln Glu Gly Trp Lys Cys Phe Arg Ile Glu Glu Ile Asp Glu Glu
225         230         235         240
Asp Val Ser Phe Leu Glu Thr Pro Lys Thr Ser Leu Glu Lys Ala Met
245         250         255
Val Asn His Leu Asp Cys Leu Thr Ser Glu Glu Glu Glu Asp Leu Lys
260         265         270
Ala Cys Leu Glu Asn Leu Asp Gln Glu Asp Ser Ile Pro Glu
275         280         285

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<210> 15

<211> 192

<212> DNA

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 15

tttgaactaa	tgtgtgatgc	cagtgattat	gcagtaggag	cagttttggg	acagaggaaa	60
gacaaggat	ttcacgcat	ctattatgct	agcaagggtcc	tgaatgaagc	acagttgaat	120
tatgcaacca	cagaaaagga	gatgctagcc	attgtctttg	ccttgagaaa	gttcagggtca	180
tacttgatag	gg					192

<210> 16

<211> 64

<212> PRT

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 16

Phe	Glu	Leu	Met	Cys	Asp	Ala	Ser	Asp	Tyr	Ala	Val	Gly	Ala	Val	Leu
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Asp His Phe His Gly Leu Leu Arg Lys Thr Pro Thr His Arg Tyr Ser
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Arg	Glu	Val	Asn	Tyr	Ile	Gly
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Tyr	Asn	Gln	Gly	Asn	Pro	Ser
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Asn	His	Glu	Pro	Pro	Gly	Phe
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<211> 1857

<212> DNA

<213> Arabidopsis thaliana

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<213> *Pisum sativum*

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<210> 26

<211> 564

<212> DNA

<213> Arabidopsis thaliana

<400> 26

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<210> 27

<211> 180

<212> DNA

<213> Arabidopsis thaliana

<400> 27

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<210> 28

<211> 192

<212> DNA

<213> Arabidopsis thaliana

<400> 28

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<210> 29

<211> 597

<212> DNA

<213> Pisum sativum

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<210> 30
 <211> 192
 <212> DNA
 <213> Pisum sativum

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 <213> Glycine max

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1362

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<211> 192

<212> DNA

<213> Glycine max

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<211> 597

<212> DNA

<213> Glycine max

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cgaacagtca ctggctggcg aatgtgtatt gactatcaca agctgaatga agctacacgg	180
aaggaccatt tccccttacc tttcatggat cagatgctgg agagacttgc agggcaggca	240
tactactgtt tcttggtatg atactcggga tacaaccaga tcgcggtaga ccccatagat	300
caggagaaga cggctctttac atgccccctt ggcgtctttg cttacagaag gatgtcattc	360
gggttatgta atgtaccagc cacatttcag aggtgcatgc tgaccatttt ttcagacatg	420
gtggagaaaa gcatcgaggt atttatggac gacttctcgg tttttggacc ctcatttgac	480
agctgtttga ggaacctaga aatggtactt cagaggtgcg tagagactaa cttggtactg	540
aattgggaaa agtgtcattt tatggttcga gagggcatag tcctaggcca caagatc	597

<210> 35

<211> 603

<212> DNA

<213> Glycine max

<400> 35

tgtgataaat gtcagagaac aaggggggata tctcgaagaa atgagatgcc tttgcagaat	60
atcatggagg tagagatctt tgatagttgg ggcatagact tcatggggcc tcttccttca	120
tcatacagga atgtctacat cttggtagct gtggattacg tctccaaatg ggtggaagcc	180
atagccacgc tgaaggacga tgccagggtg gtgatcaaat ttctgaagaa gaacattttt	240
tcccatttcg gagtcccacg agccttgatt agtgatgggg gaacgcactt ctgcaacaat	300
cagttgaaga aagtcttggg gcactataat gtccgacaca aggtggccac accttatcac	360
actcagacga atggccaagc agaaatttct aacaggggagc tcaagcgaat cctggaaaag	420
acagttgcat catcaagaaa ggattgggccc ttgaagctcg atgatactct ctgggcctat	480
aggacagcgt tcaagactcc catcggctta tcaccatttc agctagtata tgggaaggca	540
tgtcattttac cagtagagct ggagcacaag gcatattggg ctctcaagtt gctcaacttt	600
gac	603

<210> 36

<211> 150

<212> DNA

<213> Glycine max

<400> 36

cctaaaatac tacaacgaca tgattgggtg tttaggataa ttgactgaaa aacctattat	60
caatttgccg ccgttgccaa ttgggtgttt gtttggtaca tttgagattt cagacttgct	120
tagatcaagt tctttttcaa ttttcttttt	150

<210> 37
 <211> 11
 <212> DNA
 <213> Glycine max

<400> 37
 tggcgccggtt g 11

<210> 38
 <211> 15
 <212> DNA
 <213> Glycine max

<400> 38
 tggcgccggtt gccgg 15

<210> 39
 <211> 27
 <212> DNA
 <213> Glycine max

<400> 39
 tttttggcgc cggtgtcggg gattttg 27

<210> 40
 <211> 9
 <212> DNA
 <213> Glycine max

<400> 40
 tttggggga 9

<210> 41
 <211> 16
 <212> DNA
 <213> Glycine max

<400> 41
 tttaatttgg gggatt 16

<210> 42
 <211> 775
 <212> DNA
 <213> Nicotiana tabacum

<400> 42
 gtgcgtaaag aggttttttaa actggagatt atcaagtgat tggatgccgg gggttatctac 60
 cccattttacg atagttcatg aacttctccg gtgcaatgtg tcccaaagaa ggtggcatga 120
 cgggtggtcac caatgagaag aatgagttga ttcctacaag aatgggtgacc gggtggagag 180
 tgtgcatgga ctatcgcaag ctcaacaaac tcacaaggaa ggatcatttc ccatttccat 240
 tccttgacca aatgcttgat aggttggcat gtcgtgcttt ctattgcttt ctagatgtat 300
 agtcggggcta tagccaaatc tttattgctc cgtaggatca cgagaaaata cctttacatg 360
 tccctatgggt acttttgctt acaagcggat gccatttgggt ttgtgtaatg cactagcgaa 420
 ctttttatagg tgtatgatgg ctatcttcac ggacatgggt aaggactacc tttaaagtttt 480
 catggatgac ttctcgatgg ttggggattc ctttgatgat tgcttggaaa atttggataa 540
 agtattggca agatatgaag aaacgaattt ggtactaaat tgggagaagt gtcatttcat 600

gatcgaggaa ggcattgttc ttggccacaa gatctcaaat aatggcattg aagtcgacaa 660
 ggcaaagatt aagggtgattt ctaaaacttac acctccaact ttgggtgaaag gcgtgcggag 720
 tttcttaggc cagcgggggt ttaccaatt cttcataaaa gatttcacaa aggtt 775

<210> 43
 <211> 259
 <212> PRT
 <213> Nicotiana tabacum

<400> 43
 Val Arg Lys Glu Val Phe Lys Leu Glu Ile Ile Lys Glx Leu Asp Ala
 1 5 10 15
 Gly Val Ile Tyr Pro Ile Tyr Asp Ser Ser Glx Thr Ser Pro Val Gln
 20 25 30
 Cys Val Pro Lys Lys Gly Gly Met Thr Val Val Thr Asn Glu Lys Asn
 35 40 45
 Glu Leu Ile Pro Thr Arg Met Val Thr Gly Trp Arg Val Cys Met Asp
 50 55 60
 Tyr Arg Lys Leu Asn Lys Leu Thr Arg Lys Asp His Phe Pro Phe Pro
 65 70 75 80
 Phe Leu Asp Gln Met Leu Asp Arg Leu Ala Cys Arg Ala Phe Tyr Cys
 85 90 95
 Phe Leu Asp Val Glx Ser Gly Tyr Ser Gln Ile Phe Ile Ala Pro Glx
 100 105 110
 Asp His Glu Lys Thr Thr Phe Thr Cys Pro Tyr Gly Thr Phe Ala Tyr
 115 120 125
 Lys Arg Met Pro Phe Gly Leu Cys Asn Ala Leu Ala Asn Phe Tyr Arg
 130 135 140
 Cys Met Met Ala Ile Phe Thr Asp Met Val Lys Asp Tyr Leu Lys Val
 145 150 155 160
 Phe Met Asp Asp Phe Ser Met Val Gly Asp Ser Phe Asp Asp Cys Leu
 165 170 175
 Glu Asn Leu Asp Lys Val Leu Ala Arg Tyr Glu Glu Thr Asn Leu Val
 180 185 190
 Leu Asn Trp Glu Lys Cys His Phe Met Ile Glu Glu Gly Ile Val Leu
 195 200 205
 Gly His Lys Ile Ser Asn Asn Gly Ile Glu Val Asp Lys Ala Lys Ile
 210 215 220
 Lys Val Ile Ser Lys Leu Thr Pro Pro Thr Leu Val Lys Gly Val Arg
 225 230 235 240
 Ser Phe Leu Gly His Ala Gly Phe Tyr Gln Phe Phe Ile Lys Asp Phe
 245 250 255
 Thr Lys Val

<210> 44
 <211> 761
 <212> DNA
 <213> Nicotiana tabacum

<400> 44
 gtgcgtaaag aggtggtcaa gctgttggtat gtcgggggttg tgtaccccat ctctgatagc 60
 tcttgactt cgccggtgca atgtgtacca aagaagggtt gcatgactgt ggtgaaaaat 120
 tccaaaaatg agttgattcc gacaagaacc atcaccggtt ggagggtatg catggactac 180
 cgcaagttga ataaagtgac ctgcaaggat cactttcctt tgccatttct ggatcagatg 240
 ctagatcgac ttgctgggcg tgccttctat tgcttcttgg atgaatattc tgggtataac 300
 caaatcttga ttgctccgga agatccggaa aagaccacat tcacttgtcc gtatggcaca 360

tttgttttct ctaggatgcc ttttaggttg tgtaatgcac cagctacatt tcagcgggtg 420
 atgatggcca ttttctccta tatggtgaaa gacatttttg aggtgttcat ggacgatttt 480
 agtgttggg ggcactcatt tgatgaatgc ttgaagaatc ttgatagggt gttggcccat 540
 tgtgaagaaa ccaatcttgt cctcaattgg gagaaatgcc actttatggt agaagaagga 600
 atcaatctct ggcataaaat ttcaaaacat ggcattgagg tggataaaca aagatagatg 660
 tgatttcaag gctccctccc cctacatccg tcaagggagt ccgatgtttt cttgggcatg 720
 cggggttcta ttggagattc ataaaagact tctccaaggt t 761

<210> 45

<211> 254

<212> PRT

<213> Nicotiana tabacum

<400> 45

Val Arg Lys Glu Val Val Lys Leu Leu Asp Val Gly Val Val Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Ser Trp Thr Ser Pro Val Gln Cys Val Pro Lys Lys
 20 25 30
 Val Gly Met Thr Val Val Lys Asn Ser Lys Asn Glu Leu Ile Pro Thr
 35 40 45
 Arg Thr Ile Thr Gly Trp Arg Val Cys Met Asp Tyr Arg Lys Leu Asn
 50 55 60
 Lys Val Thr Cys Lys Asp His Phe Pro Leu Pro Phe Leu Asp Gln Met
 65 70 75 80
 Leu Asp Arg Leu Ala Gly Arg Ala Phe Tyr Cys Phe Leu Asp Glu Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Leu Ile Ala Pro Glu Asp Pro Glu Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Tyr Gly Thr Phe Val Phe Ser Arg Met Pro Phe
 115 120 125
 Arg Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile
 130 135 140
 Phe Ser Tyr Met Val Lys Asp Ile Phe Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Val Gly His Ser Phe Asp Glu Cys Leu Lys Asn Leu Asp Arg
 165 170 175
 Val Leu Ala His Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Glu Glu Gly Ile Asn Leu Trp His Lys Ile Ser
 195 200 205
 Lys His Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Ser Arg
 210 215 220
 Leu Pro Pro Pro Thr Ser Val Lys Gly Val Arg Cys Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Trp Arg Phe Ile Lys Asp Phe Ser Lys Val
 245 250

<210> 46

<211> 762

<212> DNA

<213> Nicotiana tabacum

<400> 46

gtgcgtaagg aggtgtttta gttgtttggat gttgggggttg tgtaccccat ctctgatagc 60
 tcttgcatatt cgccgggtgca atgtgtaccg aagaagggtg gcatgaccgt ggttgcaa 120
 tcgcaaaatg ggttgattcc taccaggatc gtcaccgggt ggaaggatg catggattac 180
 cgaaagtga ataaagtga cgcgaaggat cactttccat tgccttttct tgatcagatg 240

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ttagatcgac ttgctgggcg tgccttctac tgtttcttgg atgggtattc tggatacaac 300
caaatcttca ttactccgga agatcaggag aagacaacat tcacttgtcc atatggcacc 360
tttgcttttt ctaggatgcc ttttggggttg tgtaatgcac cgactacatt ctagcggtat 420
atgatggcca ttttctactga tatgggtggaa gatatttttg aggtgttcat ggacgacttt 480
agtgttgggt gtgattcatt tgatgaatgt ttgaataatc ttgatagagt gttggcccat 540
tgtaaagaaa ccaatcttgt tcttaattgg gagaaatgcc acttcatggt tgaggagggc 600
atagttcttg ggcataaaat tttaaagcat ggtatagagg tggacaaagc aaaaattgat 660
gtgatttcaa ggctccctcc ccctacttct gtcaaggagg tgagaagttt tcttaggcat 720
gcgggggttct accggagatt catcaaagat ttcaccaaag tt 762

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<210> 47

<211> 254

<212> PRT

<213> Nicotiana tabacum

<400> 47

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Val Arg Lys Glu Val Phe Lys Leu Leu Asp Val Gly Val Val Tyr Pro
1          5          10          15
Ile Ser Asp Ser Ser Cys Ile Ser Pro Val Gln Cys Val Pro Lys Lys
20          25          30
Gly Gly Met Thr Val Val Ala Asn Ser Gln Asn Gly Leu Ile Pro Thr
35          40          45
Arg Ile Val Thr Gly Trp Lys Val Cys Met Asp Tyr Arg Lys Leu Asn
50          55          60
Lys Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Leu Asp Gln Met
65          70          75          80
Leu Asp Arg Leu Ala Gly Arg Ala Phe Tyr Cys Phe Leu Asp Gly Tyr
85          90          95
Ser Gly Tyr Asn Gln Ile Phe Ile Thr Pro Glu Asp Gln Glu Lys Thr
100          105          110
Thr Phe Thr Cys Pro Tyr Gly Thr Phe Ala Phe Ser Arg Met Pro Phe
115          120          125
Gly Leu Cys Asn Ala Pro Thr Thr Phe Glx Arg Tyr Met Met Ala Ile
130          135          140
Phe Thr Asp Met Val Glu Asp Ile Leu Glu Val Phe Met Asp Asp Phe
145          150          155          160
Ser Val Val Gly Asp Ser Phe Asp Glu Cys Leu Asn Asn Leu Asp Arg
165          170          175
Val Leu Ala His Cys Lys Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
180          185          190
Cys His Phe Met Val Glu Glu Gly Ile Val Leu Gly His Lys Ile Leu
195          200          205
Lys His Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Ser Arg
210          215          220
Leu Pro Pro Pro Thr Ser Val Lys Gly Val Arg Ser Phe Leu Arg His
225          230          235          240
Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
245          250

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<210> 48

<211> 760

<212> DNA

<213> Nicotiana tabacum

<400> 48

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gcggaaggag gtcgtcaagc tgttggatgt cgggtgttgtg taccatcatat ttgatagctc 60
ttggactttg ccgggtgcaat atgtgccgaa gaagggtgtg atgaccgtgg ttaccaatgt 120

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aaaaaatgag	ttgattccta	ccaggactgt	caccgggtgg	agggtgtgca	tggattacca	180
caaattgaat	aaagtgaccc	gcaaggatca	ctttccatta	ccttttcttg	atcagatgtt	240
agacagactt	gctgggtgtg	ccttctactg	tttcttggat	gggtattctg	ggtgcaacaa	300
aattttgatt	gcacaaaaag	atcaggagaa	gaccaccttt	acttgtacgt	atggtacctt	360
tgtcttttct	aggatgtcat	ttgggttgtg	taatgcaccg	actacattct	agaggtgtat	420
gatggccata	tttacctaca	tggtggagga	cattttggag	gtgtttatgg	atgacttcag	480
tggtgttggt	gactagtttg	atgaatgttt	gaaaaatcct	gatagagtgt	tggcccgttg	540
tgaagaagcc	aaccttgtgc	ttaattggga	gaaatgccac	ttcatggttg	aggagggcat	600
agtccttagc	cataaaatth	caaagcatgg	tatagaggtg	gacaaagcaa	aaattgaagt	660
gatttcaagg	ctccttcccc	ctacttctgt	caagggagtt	agaagttttc	ttgggcatgc	720
ggggttctac	tggagattca	tcaaagactt	cacgaaggtt			760

<210> 49

<211> 253

<212> PRT

<213> Nicotiana tabacum

<400> 49

Arg	Lys	Glu	Val	Val	Lys	Leu	Leu	Asp	Val	Gly	Val	Val	Tyr	Pro	Ile
1				5					10					15	
Phe	Asp	Ser	Ser	Trp	Thr	Leu	Pro	Val	Gln	Tyr	Val	Pro	Lys	Lys	Gly
			20					25					30		
Gly	Met	Thr	Val	Val	Thr	Asn	Val	Lys	Asn	Glu	Leu	Ile	Pro	Thr	Arg
			35				40					45			
Thr	Val	Thr	Gly	Trp	Arg	Val	Cys	Met	Asp	Tyr	His	Lys	Leu	Asn	Lys
			50			55					60				
Val	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Leu	Asp	Gln	Met	Leu
65					70					75					80
Asp	Arg	Leu	Ala	Gly	Cys	Ala	Phe	Tyr	Cys	Phe	Leu	Asp	Gly	Tyr	Ser
			85					90						95	
Gly	Cys	Asn	Lys	Ile	Leu	Ile	Ala	Pro	Lys	Asp	Gln	Glu	Lys	Thr	Thr
			100					105					110		
Phe	Thr	Cys	Thr	Tyr	Gly	Thr	Phe	Val	Phe	Ser	Arg	Met	Ser	Phe	Gly
			115				120					125			
Leu	Cys	Asn	Ala	Pro	Thr	Thr	Phe	Glx	Arg	Cys	Met	Met	Ala	Ile	Phe
			130			135					140				
Thr	Tyr	Met	Val	Glu	Asp	Ile	Leu	Glu	Val	Phe	Met	Asp	Asp	Phe	Ser
145					150					155					160
Val	Val	Gly	Asp	Glx	Phe	Asp	Glu	Cys	Leu	Lys	Asn	Leu	Asp	Arg	Val
			165				170							175	
Leu	Ala	Arg	Cys	Glu	Glu	Ala	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys	Cys
			180				185						190		
His	Phe	Met	Val	Glu	Glu	Gly	Ile	Val	Leu	Ser	His	Lys	Ile	Ser	Lys
		195				200						205			
His	Gly	Ile	Glu	Val	Asp	Lys	Ala	Lys	Ile	Glu	Val	Ile	Ser	Arg	Leu
	210				215						220				
Leu	Pro	Pro	Thr	Ser	Val	Lys	Gly	Val	Arg	Ser	Phe	Leu	Gly	His	Ala
225					230					235					240
Gly	Phe	Tyr	Trp	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val			
			245					250							

<210> 50

<211> 762

<212> DNA

<213> Oryza sativa

<400> 50


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gtgcgtaagg aggtgtttaa gttcctgtat gccaggatta tttatctcgt accatacagc      60
gagtgggtta gcccagttca ggtcgtgccca aagaagggag gaatgacggc cgttgcaa      120
gctcaaaatg aactaatccc gcaacgaacc gtaaccggat ggagaatgtg catcgattac      180
agggaaactta acaaggctac aaaaaaggat catttccgcg tacccttcat tgatgaaatg      240
ttggaacggc tggcaaatca ttccttcttc tgtttccttg atgggtattc aggatatcat      300
caaattccca tccatccgga ggaccagagt aagactacgt tcacatgtcc atatggcacc      360
tatgcgtatc gtaggatgcc ctttggactg tgcaacactc ctgcatcttt ccaaagggtg      420
atgatgtcta ttttctcgga catgatcgag gatatcatgg aagtcttcat ggatgacttc      480
tcgggtctatg gaaagacttt gggtcattgt ctgcagaatc tagacaaagt cttacaacga      540
tgccaagaaa aggacctagt gcttaactgg gaaaagtgcc atttcatggg ctgtgaaggg      600
atagttcttg ggcacgcagt gtccgaacga ggagtcgaag ttgatcgtgc taaaattgat      660
gtgatagatc agcttccctc acccgtgaac atcaaaaggaa tccgcagctt ctttggtcac      720
gctggctttt atagaaggtt catcaaggac ttcacaaaag tt                          762

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<210> 51

<211> 254

<212> PRT

<213> Oryza sativa

<400> 51

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Val Arg Lys Glu Val Phe Lys Phe Leu Tyr Ala Arg Ile Ile Tyr Leu
  1           5           10          15
Val Pro Tyr Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
  20          25          30
Gly Gly Met Thr Ala Val Ala Asn Ala Gln Asn Glu Leu Ile Pro Gln
  35          40          45
Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
  50          55          60
Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met
  65          70          75          80
Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr
  85          90          95
Ser Gly Tyr His Gln Ile Pro Ile His Pro Glu Asp Gln Ser Lys Thr
  100         105         110
Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr Arg Arg Met Pro Phe
  115         120         125
Gly Leu Cys Asn Thr Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile
  130         135         140
Phe Ser Asp Met Ile Glu Asp Ile Met Glu Val Phe Met Asp Asp Phe
  145         150         155         160
Ser Val Tyr Gly Lys Thr Leu Gly His Cys Leu Gln Asn Leu Asp Lys
  165         170         175
Val Leu Gln Arg Cys Gln Glu Lys Asp Leu Val Leu Asn Trp Glu Lys
  180         185         190
Cys His Phe Met Val Cys Glu Gly Ile Val Leu Gly His Arg Val Ser
  195         200         205
Glu Arg Gly Val Glu Val Asp Arg Ala Lys Ile Asp Val Ile Asp Gln
  210         215         220
Leu Pro Pro Pro Val Asn Ile Lys Gly Ile Arg Ser Phe Phe Gly His
  225         230         235         240
Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
  245         250

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<210> 52

<211> 761

<212> DNA

<213> Oryza sativa

<400> 52
 gtgcgcaagg aggttttgaa attgctgcat gccaggatta tctatcccgt accatacagt 60
 gagagggtta gccaggtcca ggttgtgcca aagaaggag gaatggcggg cgttgcaa 120
 gctcagaatg aactaattac gcaacaaacc gtaaccggat ggaggatgtg tatcgattac 180
 aggaaactca acaaggctac aaaaaaggat catttcccgc tacccttcat tgttgaaatg 240
 ttggaacggc tggcaaatca ttccttcttt tgtttccttg atggatattt cggatatcat 300
 caaattccca tccatccgga ggactagagt aagactacgt tcacatgtcc atatggcacc 360
 tatgctgcat ataggatgtc ctttggactg tgcaacgctc ctgcatcttt ccaaggtgta 420
 tgatgtctat tttctcggac atgatcgagg atatcatgga agtcttcatg gatgacttct 480
 cggctctatg aaagactttc ggtcattgtc tgcaaaatct agacaaagtc ttacaacgat 540
 gccaaagaaa ggacctgggtg cttaactggg aaaagtgaca tttcatggtc cgtgaaggga 600
 tagttcttgg gcatcgagtg ttcgaacaag gaatcgaagt tgatcatgct aaaattgatg 660
 tgatagatca gcttcctcct cccgtgaaca tcaaaggat cgcagcttc ttgggtcatg 720
 tcggctttta tagaagggtc atcaaggact tcactaaagt t 761

<210> 53
 <211> 254
 <212> PRT
 <213> *Oryza sativa*

<400> 53
 Val Arg Lys Glu Val Leu Lys Leu Leu His Ala Arg Ile Ile Tyr Pro
 1 5 10 15
 Val Pro Tyr Ser Glu Arg Val Ser Pro Val Gln Val Val Pro Lys Lys
 20 25 30
 Gly Gly Met Ala Val Val Ala Asn Ala Gln Asn Glu Leu Ile Thr Gln
 35 40 45
 Gln Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
 50 55 60
 Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Val Glu Met
 65 70 75 80
 Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr
 85 90 95
 Phe Gly Tyr His Gln Ile Pro Ile His Pro Glu Asp Glx Ser Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr His Arg Met Ser Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile
 130 135 140
 Phe Ser Asp Met Ile Glu Asp Ile Met Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Tyr Gly Lys Thr Phe Gly His Cys Leu Gln Asn Leu Asp Lys
 165 170 175
 Val Leu Gln Arg Cys Gln Glu Lys Asp Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Glx His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Arg Val Phe
 195 200 205
 Glu Gln Gly Ile Glu Val Asp His Ala Lys Ile Asp Val Ile Asp Gln
 210 215 220
 Leu Pro Pro Pro Val Asn Ile Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 54
 <211> 762

<212> DNA

<213> Oryza sativa

<400> 54

gtgcggaag	aggtttttaa	gctcctgcat	gccgggatta	tttataccgt	tccatgcagt	60
gagtggtca	gcacagtcca	ggttgggccg	aagatgggat	gaatgacggt	cgttgcaa	120
gctcaaaata	aacttatccc	gcaaccaacc	ataaccggat	ggaggatgtg	catagactac	180
aggaaactca	acaaggctac	aaaagaggat	cattttccgc	tacccttcat	tgatgaaatg	240
ttggaacgga	tgacaaatca	ttcctttcttc	tgtttccttg	atgggtattc	cggatatcat	300
caaattccca	tcggtccaga	ggaccagagt	aagactacgt	tcacatgtcc	atatggcacc	360
tatgcgtatc	gtaggatgtc	cttcggactg	tgcaacgctc	ctgcatcttt	ccaaaggtgt	420
atgttgtcta	ttttctcgga	catgatcgaa	gatatcatga	aagtcttcat	ggatgacttc	480
tcagtttatg	gaaagacttt	cggtcatttg	ctgtagaatc	tagacaaagt	cttacaacga	540
tgccaagaaa	atgacctagt	gtttaattgg	gaaaagtgcc	attttatggg	ccgtgaaggg	600
atagttcttg	ggcatcgagt	atccgaatga	ggaatcgaag	ttgatcgtgc	taaaatcgat	660
gttatagatc	aaattcgtcc	tcctgcgaat	atcaaaggaa	tccgcagctt	cttggggacat	720
gccggccttt	atagaagggt	cctcaaggac	ttcacaaaag	tt		762

<210> 55

<211> 254

<212> PRT

<213> Oryza sativa

<400> 55

Val	Arg	Lys	Glu	Val	Phe	Lys	Leu	Leu	His	Ala	Gly	Ile	Ile	Tyr	Thr
1				5					10					15	
Val	Pro	Cys	Ser	Glu	Trp	Val	Ser	Thr	Val	Gln	Val	Gly	Pro	Lys	Met
			20					25					30		
Gly	Glx	Met	Thr	Val	Val	Ala	Asn	Ala	Gln	Asn	Lys	Leu	Ile	Pro	Gln
		35					40					45			
Pro	Thr	Ile	Thr	Gly	Trp	Arg	Met	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn
	50					55				60					
Lys	Ala	Thr	Lys	Glu	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Glu	Met
65					70					75				80	
Leu	Glu	Arg	Met	Thr	Asn	His	Ser	Phe	Phe	Cys	Phe	Leu	Asp	Gly	Tyr
				85					90					95	
Ser	Gly	Tyr	His	Gln	Ile	Pro	Ile	Arg	Pro	Glu	Asp	Gln	Ser	Lys	Thr
			100					105					110		
Thr	Phe	Thr	Cys	Pro	Tyr	Gly	Thr	Tyr	Ala	Tyr	Arg	Arg	Met	Ser	Phe
		115					120					125			
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Ser	Phe	Gln	Arg	Cys	Met	Leu	Ser	Ile
	130					135					140				
Phe	Ser	Asp	Met	Ile	Glu	Asp	Ile	Met	Lys	Val	Phe	Met	Asp	Asp	Phe
145					150					155					160
Ser	Val	Tyr	Gly	Lys	Thr	Phe	Gly	His	Cys	Leu	Glx	Asn	Leu	Asp	Lys
				165					170					175	
Val	Leu	Gln	Arg	Cys	Gln	Glu	Asn	Asp	Leu	Val	Phe	Asn	Trp	Glu	Lys
			180					185					190		
Cys	His	Phe	Met	Val	Arg	Glu	Gly	Ile	Val	Leu	Gly	His	Arg	Val	Ser
		195					200					205			
Glu	Glx	Gly	Ile	Glu	Val	Asp	Arg	Ala	Lys	Ile	Asp	Val	Ile	Asp	Gln
	210					215					220				
Ile	Arg	Pro	Pro	Ala	Asn	Ile	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His
225					230					235					240
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Leu	Lys	Asp	Phe	Thr	Lys	Val		
				245					250						

<210> 56
 <211> 762
 <212> DNA
 <213> Oryza sativa

<400> 56
 gtgcgtaagg aggtcttgaa gctcttgcat gccgagatta tttatcccgt accatataga 60
 gaggtagggtta gcccgggtcta gggtatgccg aagaagggac gaatgacggg cattgcaaatt 120
 gctcaaaatg aacttattcc gcaacgaaca gtaaccggat ggaggatgtg catagattac 180
 atgaaactta acaaggctac gaaaaaggat catttcccac tacccttcat tgatgaaatg 240
 ttggaacggc tggcaaatca ttctttcttc cgtttccttg atgggtattc taggtatgat 300
 caaattccca tccatccgga ggaccaaaagt aagactacgt tcacatgttc gtatgatacc 360
 tatgcttata gtaggatgtc cttcggactg tgcaacgctc ctgcatcttt ccaaagggtg 420
 atgatgtcta ttttctccga catgattaag gacattatgg aagtcttcat gcatgacttc 480
 tctatttatg gaaagacctc cggtcattgt ctacaaaatt tagacaaaat tttgcaacga 540
 tgccaagaga aggacctggg acttaattgg gaaaagtgtc atttcatggg cagtgaagg 600
 atagttctta gtcacgcagt gtccgaataa ggaatcgaag ttgatcgtgc taaaaactat 660
 gtaatagatt agcttccttc tcctgtgaac attaagggga tccgcaattt tttgggacat 720
 gctggccttt atagaagggt catcaaagac ttcacaaagg tt 762

<210> 57
 <211> 254
 <212> PRT
 <213> Oryza sativa

<400> 57
 Val Arg Lys Glu Val Leu Lys Leu Leu His Ala Glu Ile Ile Tyr Pro
 1 5 10 15
 Val Pro Tyr Arg Glu Trp Val Ser Pro Val Glx Val Met Pro Lys Lys
 20 25 30
 Gly Arg Met Thr Val Ile Ala Asn Ala Gln Asn Glu Leu Ile Pro Gln
 35 40 45
 Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Met Lys Leu Asn
 50 55 60
 Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met
 65 70 75 80
 Leu Glu Arg Leu Ala Asn His Ser Phe Phe Arg Phe Leu Asp Gly Tyr
 85 90 95
 Ser Arg Tyr Asp Gln Ile Pro Ile His Pro Glu Asp Gln Ser Lys Thr
 100 105 110
 Thr Phe Thr Cys Ser Tyr Asp Thr Tyr Ala Tyr Arg Arg Met Ser Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile
 130 135 140
 Phe Ser Asp Met Ile Lys Asp Ile Met Glu Val Phe Met His Asp Phe
 145 150 155 160
 Ser Ile Tyr Gly Lys Thr Ser Gly His Cys Leu Gln Asn Leu Asp Lys
 165 170 175
 Ile Leu Gln Arg Cys Gln Glu Lys Asp Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Arg Glu Gly Ile Val Leu Ser His Arg Val Ser
 195 200 205
 Glu Glx Gly Ile Glu Val Asp Arg Ala Lys Asn Tyr Val Ile Asp Glx
 210 215 220
 Leu Pro Ser Pro Val Asn Ile Lys Gly Ile Arg Asn Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val

245

250

<210> 58
 <211> 762
 <212> DNA
 <213> Hordeum vulgare

<400> 58
 gtgcgcaagg aggttttagaa gttcctggaa gcaggtatca tctatcgtgt tgctcatagt 60
 gattggttga gtcgggtgca ttgtgtccct aagaaggag gcattaccgt tgccctaata 120
 gataaggatg aattgatccc acagaggact attactggct ataggatggg gattgatttt 180
 aggaaattga ataaagccac taggaaagat cattaccctt tgccttttat cgaccaaata 240
 cgagaaaggc tgtctaaaca cacacacttc tgctttctaa acggttatTTt tggtttctcc 300
 caaataaccag ttgcacaatc tgatcaggag aaaaccactt tcacctgccc ttttggtaca 360
 tttgcttata gacgtatgac ttttggttta tgtaatgcac ctgcctcctt tcaaagatgt 420
 atgatggcta tattccctga cttttgtgaa aagattgttg aggttttcat ggatgacttc 480
 tccatttacg gatcttccctt tgatgattgc ctcagcaacc ttgatcgagt cttgcagaga 540
 tgtaaagaca ccaatctttt cttgaattgg aagaagtgcc actttatggg taatgacggc 600
 atcgtcttag gacataaatt ttctgaaaga ggtattgaag tcgataaggc taaggttgat 660
 ggaatcgaga aaatgccata cccacagat atcaaaggga taagaagttt ccttggtcat 720
 gctggtttct atagaagggt cataaaagac ttcactaagg tt 762

<210> 59
 <211> 254
 <212> PRT
 <213> Hordeum vulgare

<400> 59
 Val Arg Lys Glu Val Glx Lys Phe Leu Glu Ala Gly Ile Ile Tyr Arg
 1 5 10 15
 Val Ala His Ser Asp Trp Leu Ser Arg Val His Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln
 35 40 45
 Arg Thr Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn
 50 55 60
 Lys Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80
 Arg Glu Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asn Gly Tyr
 85 90 95
 Phe Gly Phe Ser Gln Ile Pro Val Ala Gln Ser Asp Gln Glu Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Thr Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ala Ile
 130 135 140
 Phe Pro Asp Phe Cys Glu Lys Ile Val Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Ile Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg
 165 170 175
 Val Leu Gln Arg Cys Lys Asp Thr Asn Leu Phe Leu Asn Trp Lys Lys
 180 185 190
 Cys His Phe Met Val Asn Asp Gly Ile Val Leu Gly His Lys Phe Ser
 195 200 205
 Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Gly Ile Glu Lys
 210 215 220
 Met Pro Tyr Pro Thr Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His

<400>	60
gtgcgtaaag aggtcctaaa gttcctggaa gcgggtatta tctatcctgt tgctcacaac	60
gattgggtga gtccgggtgca ttgcgtccct aagaagggat gcattaccgt tgtccctaata	120
gataaggatg aattgatccc acataggatt attactggct ataggatggt gatcgattttt	180
aggaaaatga ataaagccac taggaaagaa cattaccctt tgaccttttag cgaccaaatg	240
ctagaaaggt tgtctaaaca cacacacttc tgctttctag acggttatcc tagttttctcc	300
caaatactag ttgcacaatc tgatcaggag aaaaccactt tcacctaccc gttcgggtacc	360
tttgcttata gaagtatgcc ttttggttta tgtaatgcac ctgccacctt tcaaagatgt	420
atgatggcta tattctctga cttttgtgaa aagtttgtcg aggttttcat ggatgacttt	480
tccgtttacg gatcttcctt tgatgattgc ctcaacaacc ttgatcgggt cttgcagaga	540
tgtaaaagata ctaatcttgt cttgaattgg gagaagtgcc actttatggt taatgaaggc	600
atcgtcttag gacataaaat ttccgaaaga ggtattgaat tcgataaggc taaggttgggt	660
gcaatcaaga aaatgccata cccacagat atcaaaggta taagaagttt cttggtccat	720
gctgqgtttct atagaagggt catcaaggac ttacaaaagg tt	762

<400>	61																
Val	Arg	Lys	Glu	Val	Leu	Lys	Phe	Leu	Glu	Ala	Gly	Ile	Ile	Tyr	Pro		
1				5					10					15			
Val	Ala	His	Asn	Asp	Trp	Val	Ser	Pro	Val	His	Cys	Val	Pro	Lys	Lys		
			20					25					30				
Gly	Cys	Ile	Thr	Val	Val	Pro	Asn	Asp	Lys	Asp	Glu	Leu	Ile	Pro	His		
		35					40					45					
Arg	Ile	Ile	Thr	Gly	Tyr	Arg	Met	Val	Ile	Asp	Phe	Arg	Lys	Met	Asn		
	50					55					60						
Lys	Ala	Thr	Arg	Lys	Glu	His	Tyr	Pro	Leu	Pro	Phe	Ser	Asp	Gln	Met		
65					70					75				80			
Leu	Glu	Arg	Leu	Ser	Lys	His	Thr	His	Phe	Cys	Phe	Leu	Asp	Gly	Tyr		
				85					90					95			
Ser	Ser	Phe	Ser	Gln	Ile	Leu	Val	Ala	Gln	Ser	Asp	Gln	Glu	Lys	Thr		
			100					105					110				
Thr	Phe	Thr	Tyr	Pro	Phe	Gly	Thr	Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe		
		115					120					125					
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Met	Ala	Ile		
	130					135					140						
Phe	Ser	Asp	Phe	Cys	Glu	Lys	Phe	Val	Glu	Val	Phe	Met	Asp	Asp	Phe		
145				150					155					160			
Ser	Val	Tyr	Gly	Ser	Ser	Phe	Asp	Asp	Cys	Leu	Asn	Asn	Leu	Asp	Arg		
				165					170					175			
Val	Leu	Gln	Arg	Cys	Lys	Asp	Thr	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys		
			180					185					190				
Cys	His	Phe	Met	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Ile	Ser		
		195					200					205					
Glu	Arg	Gly	Ile	Glu	Phe	Asp	Lys	Ala	Lys	Val	Gly	Ala	Ile	Lys	Lys		

210 215 220
 Met Pro Tyr Pro Thr Asp Ile Lys Gly Ile Arg Ser Phe Leu Val His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 62
 <211> 757
 <212> DNA
 <213> Hordeum vulgare

<400> 62
 gaaaagaggt tgtgaagctc ctggatgaag gtattatcta tcatgttgct catagcgatt 60
 gggtagagtc ggtgcatagc gttcctaaga agggaggcat taccgttgct cctaatagata 120
 aggatgaatt gatcccgagc aggattatca ctggctatag gatggatgac gatttcagga 180
 aactgaataa agccactagg aaagatcatt accctttgcc tttatcgac catatgctag 240
 aaaggttgtc caaactcaca cacttctgct ttctagacgg ttattctagt ttctcccaaa 300
 taccagttgc acaatctgat caggagaaaa ccactttcac ctgccctttc ggtacctttg 360
 cttatagacg tatgcctttt ggcttatgta atgcacctgc cacctttcaa agatgtatga 420
 tggctatatt ctctaacttt tgtgaaaata ttgtcgaggt tttcatggat gacttttccg 480
 tttacgggctc ttcttttgat gattgcctca gcaaccttga tcgagtctta cagagatgta 540
 aagacaccaa tcttgtcttg aatggggaga agtgccactt tatggttaat gaaggcatcg 600
 tcttaggaca taaaatttct gaaagaggta ttgaagtcga taaggctaag gttgatgcaa 660
 tcgacaaaat gccatacccc acagatatca aaggataaag aagtttcctt ggtcatgggtg 720
 gtttctatag aaggtttatc aaagatttca caaaggt 757

<210> 63
 <211> 251
 <212> PRT
 <213> Hordeum vulgare

<400> 63
 Lys Glu Val Val Lys Leu Leu Asp Glu Gly Ile Ile Tyr His Val Ala
 1 5 10 15
 His Ser Asp Trp Val Ser Pro Val His Ser Val Pro Lys Lys Gly Gly
 20 25 30
 Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln Arg Ile
 35 40 45
 Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn Lys Ala
 50 55 60
 Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Ile Asp His Met Leu Glu
 65 70 75 80
 Arg Leu Ser Lys Leu Thr His Phe Cys Phe Leu Asp Gly Tyr Ser Ser
 85 90 95
 Phe Ser Gln Ile Pro Val Ala Gln Ser Asp Gln Glu Lys Thr Thr Phe
 100 105 110
 Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe Gly Leu
 115 120 125
 Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile Phe Ser
 130 135 140
 Asn Phe Cys Glu Asn Ile Val Glu Val Phe Met Asp Asp Phe Ser Val
 145 150 155 160
 Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg Val Leu
 165 170 175
 Gln Arg Cys Lys Asp Thr Asn Leu Val Leu Asn Gly Glu Lys Cys His
 180 185 190
 Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser Glu Arg

Gly	Ile	Glu	Val	Asp	Lys	Ala	Lys	Val	Asp	Ala	Ile	Asp	Lys	Met	Pro	
	210					215					220					
Tyr	Pro	Thr	Asp	Ile	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His	Gly	Gly	
225					230					235					240	
Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys						
				245					250							

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<210> 64
<211> 740
<212> DNA
<213> Hordeum vulgare
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[illegible]

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<210> 65
<211> 247
<212> PRT
<213> Hordeum vulgare
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<400>	65																
Val	Arg	Lys	Glu	Val	Ile	Lys	Phe	Leu	Glu	Glu	Gly	Ile	Ile	Tyr	Pro		
1				-5					10					15			
Val	Ala	His	Ser	Asp	Trp	Val	Ser	Pro	Val	His	Cys	Ile	Pro	Lys	Lys		
			20					25					30				
Gly	Gly	Ile	Thr	Val	Val	Pro	Asn	Asp	Lys	Asp	Glu	Leu	Ile	Pro	Glx		
		35					40					45					
Arg	Ile	Ile	Thr	Gly	Tyr	Arg	Met	Val	Ile	Asp	Phe	Arg	Lys	Leu	Asn		
	50					55					60						
Lys	Ala	Thr	Arg	Lys	Asp	His	Tyr	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met		
65					70					75					80		
Leu	Glu	Arg	Leu	Ser	Lys	His	Thr	His	Phe	Leu	Phe	Leu	Asp	Gly	Tyr		
			85						90					95			
Thr	Gly	Phe	Ser	Gln	Ile	Pro	Val	Ala	Gln	Phe	Asp	Gln	Glu	Lys	Thr		
			100					105					110				
Thr	Leu	Thr	Glx	His	Phe	Gly	Thr	Phe	Ala	Tyr	Ile	Arg	Met	Pro	Phe		
		115					120					125					
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Met	Ala	Ile		
	130					135					140						
Phe	Ser	Asp	Phe	Cys	Glu	Lys	Ile	Val	Asn	Val	Phe	Met	Asp	Asn	Phe		
145					150					155					160		
Ser	Val	Tyr	Gly	Cys	Ser	Phe	Asp	Asp	Cys	Leu	Asn	Asn	Val	Asp	Arg		
				165					170					175			
Val	Leu	Gln	Arg	Cys	Lys	Asp	Thr	Asn	Val	Val	Leu	Asn	Trp	Glu	Lys		

180 185 190
 Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser
 195 200 205
 Glu Arg Gly Ile Lys Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys
 210 215 220
 Met Pro Tyr Pro Thr Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe
 245

<210> 66
 <211> 762
 <212> DNA
 <213> Avena sativa

<400> 66
 gtgcgaaagg aggttttcaa gctcatggat gctgggtatta ttaccctat tgctgatagt 60
 gaatgggtta gtcattgttca ttgtgttcct aaaaaggagg gtattaccgt tgtccctaata 120
 gataatgatg agcttattcc tcaaagaata gtggtaggct ataggatgtg catcgatttt 180
 aggaaagtca ataaagttac taagaaagat cactaccgcg ttccttttat tgatcaaagt 240
 ttggaaagat tttctaaaaa gaccattttt tgttttcttg atggttattc tggtttctct 300
 caaattgttg ttaaacaaca agatcaagaa aaaactactt ttacttgccc ttatggaact 360
 tatgcttata gatgtatgcc ttttgggtta tgtaatgtc cttctacttt cctaagggtgc 420
 atgtctgcta tctttcatgg ttttgtgtg gaaattgtag aagtgttcat ggacgacttt 480
 tctgtctacg gaacttcttt tgataattgt ctgcacaacc ttgataaagt tttacagaga 540
 tgtgaaggaa ctaattctgt tcttaattgg gagaaatgcc acttcatggg taatgaaggg 600
 attgttcttg ggcataaagt ttctaaaaga ggcataagaag ttgatagagc taagggttgag 660
 gcaattgaga agatgccatg tccaagagac atcaaaggta ttcgtagtat ccttggtcat 720
 gctgggttct ataggagggt catcaaagac ttcacaaagg tt 762

<210> 67
 <211> 254
 <212> PRT
 <213> Avena sativa

<400> 67
 Val Arg Lys Glu Val Phe Lys Leu Met Asp Ala Gly Ile Ile Tyr Pro
 1 5 10 15
 Ile Ala Asp Ser Glu Trp Val Ser His Val His Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Ile Thr Val Val Pro Asn Asp Asn Asp Glu Leu Ile Pro Gln
 35 40 45
 Arg Ile Val Val Gly Tyr Arg Met Cys Ile Asp Phe Arg Lys Val Asn
 50 55 60
 Lys Val Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Glu Arg Phe Ser Lys Lys Thr His Phe Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Phe Ser Gln Ile Val Val Lys Gln Gln Asp Gln Glu Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr Arg Cys Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ser Thr Phe Leu Arg Cys Met Ser Ala Ile
 130 135 140
 Phe His Gly Phe Cys Glu Glu Ile Val Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Tyr Gly Thr Ser Phe Asp Asn Cys Leu His Asn Leu Asp Lys

				165				170					175			
Val	Leu	Gln	Arg	Cys	Glu	Gly	Thr	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys	
			180					185					190			
Cys	His	Phe	Met	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Val	Ser	
		195					200					205				
Lys	Arg	Gly	Ile	Glu	Val	Asp	Arg	Ala	Lys	Val	Glu	Ala	Ile	Glu	Lys	
	210					215					220					
Met	Pro	Cys	Pro	Arg	Asp	Ile	Lys	Gly	Ile	Arg	Ser	Ile	Leu	Gly	His	
225					230					235					240	
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val			
				245					250							

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<210> 68
<211> 762 ..
<212> DNA
<213> Avena sativa
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<400> 68						
gtgcgcaaag	aggtctttaa	gttccttgat	gctgggtatta	tttaccctat	tgctgatagt	60
caatgggtta	gccttggtca	ttgtgtcccc	aagaaagggg	gaataactgt	tgtgcctaata	120
gaagataatg	agcttatacc	ccaaagagta	gtggttggtg	atagaatgtg	cattgatttt	180
agaaggatta	ataaagttac	taggaaagat	cattatcctt	tgccctttat	tgatcaaata	240
cttgagaggt	tgtccaaaaa	gactcacttt	tgttttcttg	atgggtcattc	tgggtttttct	300
caaattggtg	tgaaagcaca	agaccaagag	aaaactactt	tcacttgctc	ttatggtact	360
tatgattata	ggcgtatgcc	ttttgggtta	tgtaatgtct	ctgctacctt	tcagagatgt	420
atgtctgcta	tatttcatgg	tttttggtga	gaaattgtgg	aggttttcat	ggacgatttt	480
tctgtctatg	gaacttcttt	tgataactgt	ttgcacaacc	ttgataaaatt	tttgcagaga	540
tttgaagaaa	ccaaccttgt	tcttaattgg	gagaaatgcc	atttcatggg	taatgaaggg	600
attgttcttg	gacacaagat	ctcagaaaaga	ggcattgaag	ttgacagagc	caaaattgaa	660
gcaattgaga	acatgccttg	ccctagagat	attaaaggta	ttcgtagtat	ccttggtcat	720
qctggtttct	atagtaggtt	catcaaagac	tttacaaaag	tt		762

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<210> 69 .....
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<211> 254
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```
<212> PRT
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```
<213> Avena sativa
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<400> 69																
Val	Arg	Lys	Glu	Val	Phe	Lys	Phe	Leu	Asp	Ala	Gly	Ile	Ile	Tyr	Pro	
1				5					10					15		
Ile	Ala	Asp	Ser	Gln	Trp	Val	Ser	Leu	Val	His	Cys	Val	Pro	Lys	Lys	
			20					25					30			
Gly	Gly	Ile	Thr	Val	Val	Pro	Asn	Glu	Asp	Asn	Glu	Leu	Ile	Pro	Gln	
		35					40					45				
Arg	Val	Val	Val	Val	Tyr	Arg	Met	Cys	Ile	Asp	Phe	Arg	Arg	Ile	Asn	
	50					55					60					
Lys	Val	Thr	Arg	Lys	Asp	His	Tyr	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met	
65					70					75					80	
Leu	Glu	Arg	Leu	Ser	Lys	Lys	Thr	His	Phe	Cys	Phe	Leu	Asp	Gly	His	
				85					90					95		
Ser	Gly	Phe	Ser	Gln	Ile	Val	Val	Lys	Ala	Gln	Asp	Gln	Glu	Lys	Thr	
			100					105					110			
Thr	Phe	Thr	Cys	Pro	Tyr	Gly	Thr	Tyr	Asp	Tyr	Arg	Arg	Met	Pro	Phe	
		115					120					125				
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Ser	Ala	Ile	
	130					135					140					
Phe	His	Gly	Phe	Cys	Glu	Glu	Ile	Val	Glu	Val	Phe	Met	Asp	Asp	Phe	

145 150 155 160
 Ser Val Tyr Gly Thr Ser Phe Asp Asn Cys Leu His Asn Leu Asp Lys
 165 170 175
 Phe Leu Gln Arg Phe Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser
 195 200 205
 Glu Arg Gly Ile Glu Val Asp Arg Ala Lys Ile Glu Ala Ile Glu Asn
 210 215 220
 Met Pro Cys Pro Arg Asp Ile Lys Gly Ile Arg Ser Ile Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Ser Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 70

<211> 756

<212> DNA

<213> Avena sativa

<400> 70

aaggagggttt	ttaaactcct	tgatggttgg	attatattacc	ctattgctga	tagtgaatgg	60
gtagtcttgg	ttcattgtgt	tcctaaaaag	ggaggtatta	ccgttggtcc	taatgataat	120
gatgagctta	ttcctcaaag	aatagtggta	ggctatagga	tgtgcataga	ttttaggaaa	180
gttaataaag	ttactaagaa	agatcactac	ccgcttcctt	ttattgatca	aatgttggaa	240
agggtgtcta	aaaagacca	tttttgtttt	cttgatgggt	actctagctt	ctctcaaatt	300
gctgttaaac	aacaagatca	agaaaaaact	acttttactt	gcccttatgg	aacttttgct	360
tatagacgta	tgctattgg	tttatgtaat	gctcctgcta	cttttcaaag	gtgtatgtct	420
gctatatttc	atgggttttg	tgaggaaatt	gtagaagtgt	tcatggatga	cttttctgtc	480
tatggaactt	cttttgataa	ttgcctgcac	aaccttgata	aagttttgca	gagatgtgaa	540
gaaactaata	ttgttcttaa	ttggggagaaa	ttccacttca	tggttaatga	agggattgtc	600
cttgggcata	aagtttctaa	aagaggcata	gaagttgata	gagctaaggt	tgaggcaatt	660
gagaagatgc	catgcccaag	agacatcaaa	ggtatacgta	gtatccttgg	tcatgctggg	720
ttctatagaa	ggtttatcaa	agacttcaca	aaggtt			756

<210> 71

<211> 252

<212> PRT

<213> Avena sativa

<400> 71

Lys	Glu	Val	Phe	Lys	Leu	Leu	Asp	Val	Gly	Ile	Ile	Tyr	Pro	Ile	Ala
1				5					10					15	
Asp	Ser	Glu	Trp	Val	Ser	Leu	Val	His	Cys	Val	Pro	Lys	Lys	Gly	Gly
				20				25						30	
Ile	Thr	Val	Val	Pro	Asn	Asp	Asn	Asp	Glu	Leu	Ile	Pro	Gln	Arg	Ile
				35				40						45	
Val	Val	Gly	Tyr	Arg	Met	Cys	Ile	Asp	Phe	Arg	Lys	Val	Asn	Lys	Val
				50				55						60	
Thr	Lys	Lys	Asp	His	Tyr	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met	Leu	Glu
65					70					75				80	
Arg	Leu	Ser	Lys	Lys	Thr	His	Phe	Cys	Phe	Leu	Asp	Gly	Tyr	Ser	Ser
				85					90					95	
Phe	Ser	Gln	Ile	Ala	Val	Lys	Gln	Gln	Asp	Gln	Glu	Lys	Thr	Thr	Phe
				100					105					110	
Thr	Cys	Pro	Tyr	Gly	Thr	Phe	Ala	Tyr	Arg	Arg	Met	Pro	Ile	Gly	Leu
				115					120					125	
Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Ser	Ala	Ile	Phe	His

	130				135				140						
Gly	Phe	Cys	Glu	Glu	Ile	Val	Glu	Val	Phe	Met	Asp	Asp	Phe	Ser	Val
145					150					155					160
Tyr	Gly	Thr	Ser	Phe	Asp	Asn	Cys	Leu	His	Asn	Leu	Asp	Lys	Val	Leu
				165					170					175	
Gln	Arg	Cys	Glu	Glu	Thr	Asn	Ile	Val	Leu	Asn	Trp	Glu	Lys	Phe	His
			180					185					190		
Phe	Met	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Val	Ser	Lys	Arg
		195				200						205			
Gly	Ile	Glu	Val	Asp	Arg	Ala	Lys	Val	Glu	Ala	Ile	Glu	Lys	Met	Pro
	210				215						220				
Cys	Pro	Arg	Asp	Ile	Lys	Gly	Ile	Arg	Ser	Ile	Leu	Gly	His	Ala	Gly
225				230					235						240
Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val				
				245				250							

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<210> 72
<211> 748
<212> DNA
<213> Secale cereale
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<400>	72						
gtgcggaag	aggctcttaa	actcctagag	gcagggtatta	actatcccat	tgctgatagc		60
cagcgggtaa	gtcatgtcca	tttgtgttcct	aagaaaggag	gtatgactgt	cgtccctaag		120
gataaagatg	aatttatccc	gcaaagaata	gttacagggt	ataggatggt	aattgatttt		180
cgtaagttaa	ataaagctac	tatgaaagat	cattaccacct	tgccatttat	tgatcaaata		240
ccagacaggt	tatccaaaca	tactcatttc	tgcttttctag	atgggtattc	tggtttctct		300
caaatacctt	tgtcaaaggg	ggatcaagaa	aagaccacct	ttacttgtcc	tttcggtacc		360
tttgcttata	gaggatatgcc	ttttgggttta	tgtaatgcac	ctgctacctt	tcaaagatgt		420
atgatcgтта	tattctctgt	cttttttgaa	aagattgttg	aggattccat	ggatgatttc		480
tccgttttatg	gaacttcttt	tgatatttgc	ttaagcaacc	ttgatcgagt	tttgacagaga		540
tgtgaagata	ctaaccctgt	cttgaattgg	gagaagtgcc	actttatggt	taatgaaggc		600
attttcttgg	gacataaaat	ttctgaaaaga	ggtagtgaa	ttgagaaagc	taaagtggat		660
gctattgaaa	agatgccatg	ccctaaggat	atgaaaggta	tacgaagttt	ccttggtcac		720
qctqqgtttt	ataggagggt	cataaaag					748

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<210> 73
<211> 249
<212> PRT
<213> Secale cereale
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<400> 73															
Val	Arg	Lys	Glu	Val	Phe	Lys	Leu	Leu	Glu	Ala	Gly	Ile	Asn	Tyr	Pro
1				5					10					15	
Ile	Ala	Asp	Ser	Gln	Arg	Val	Ser	His	Val	His	Cys	Val	Pro	Lys	Lys
				20				25					30		
Gly	Gly	Met	Thr	Val	Val	Pro	Lys	Asp	Lys	Asp	Glu	Phe	Ile	Pro	Gln
		35					40					45			
Arg	Ile	Val	Thr	Gly	Tyr	Arg	Met	Val	Ile	Asp	Phe	Arg	Lys	Leu	Asn
	50					55					60				
Lys	Ala	Thr	Met	Lys	Asp	His	Tyr	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met
65					70					75				80	
Pro	Asp	Arg	Leu	Ser	Lys	His	Thr	His	Phe	Cys	Phe	Leu	Asp	Gly	Tyr
				85					90					95	
Ser	Gly	Phe	Ser	Gln	Ile	Pro	Leu	Ser	Lys	Gly	Asp	Gln	Glu	Lys	Thr
			100					105					110		
Thr	Phe	Thr	Cys	Pro	Phe	Gly	Thr	Phe	Ala	Tyr	Arg	Gly	Met	Pro	Phe

115 120 125
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Ile Val Ile
 130 135 140
 Phe Ser Val Phe Phe Glu Lys Ile Val Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Tyr Gly Thr Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg
 165 170 175
 Val Leu Gln Arg Cys Glu Asp Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Asn Glu Gly Ile Phe Leu Gly His Lys Ile Ser
 195 200 205
 Glu Arg Gly Thr Glu Val Glu Lys Ala Lys Val Asp Ala Ile Glu Lys
 210 215 220
 Met Pro Cys Pro Lys Asp Met Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys
 245

<210> 74
 <211> 762
 <212> DNA
 <213> Secale cereale

<400> 74
 gtgcggaagg aggtcggttaa gcttccagag gcaggtatta tctatcccgt tgctgatagc 60
 cagtgggttaa gtcattgtcca ttgtgtccct aagaagggag gtatgactgt cgttcctaata 120
 gacaaacatg aattgatccc gcaaagaata gttacagggt ataggatggg aattgatttc 180
 cgtaagttaa ataaagctac taagaaagat cattaccctt tgccatttat tgatcaaagt 240
 ctagacaggt tatccaaaca tactcatttt tgctttctag atggttatta tggtttctct 300
 caaataacctg tgtcaaaagg ggatcaagaa aagaccactt tcacttggtc tttcgggtacc 360
 tttgcttata gacgtatgcc ttttggttta tgtaatgcac ctgctacctt tcaaagatgt 420
 atgatggcta tattatctga tttttgagaa aagattggtt aggttttcat ggatgatttc 480
 tccgtttacg gaacttcttt tgatgactac ttaagcaaca atgacgagt tttgcagaga 540
 tgtgaagaca ctaattctgt tttgaattgg gagaagtgcc actttatggt taatgaaggc 600
 attgtcttgg gacaaaaaat ttctgaaaga ggtattgaag ttgacaaagc taaagtcgat 660
 gctgttgaaa agatgccatg cccaaggac atcaaaggta tacgaagttt ccttggtcat 720
 gttgggtttt ataggaggtt catcaaagac ttcacgaaag tt 762

<210> 75
 <211> 254
 <212> PRT
 <213> Secale cereale

<400> 75
 Val Arg Lys Glu Val Val Lys Leu Pro Glu Ala Gly Ile Ile Tyr Pro
 1 5 10 15
 Val Ala Asp Ser Gln Trp Val Ser His Val His Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Val Pro Asn Asp Lys His Glu Leu Ile Pro Gln
 35 40 45
 Arg Ile Val Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn
 50 55 60
 Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Asp Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asp Gly Tyr
 85 90 95
 Tyr Gly Phe Ser Gln Ile Pro Val Ser Lys Gly Asp Gln Glu Lys Thr

			100					105				110			
Thr	Phe	Thr	Cys	Pro	Phe	Gly	Thr	Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe
		115					120					125			
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Met	Ala	Ile
	130					135					140				
Leu	Ser	Asp	Phe	Glx	Glu	Lys	Ile	Val	Glu	Val	Phe	Met	Asp	Asp	Phe
145					150					155					160
Ser	Val	Tyr	Gly	Thr	Ser	Phe	Asp	Asp	Tyr	Leu	Ser	Asn	Asn	Asp	Arg
			165					170						175	
Val	Leu	Gln	Arg	Cys	Glu	Asp	Thr	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys
		180						185					190		
Cys	His	Phe	Met	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	Gln	Lys	Ile	Ser
		195					200					205			
Glu	Arg	Gly	Ile	Glu	Val	Asp	Lys	Ala	Lys	Val	Asp	Ala	Val	Glu	Lys
	210					215					220				
Met	Pro	Cys	Pro	Lys	Asp	Ile	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His
225					230					235					240
Val	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
			245						250						

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<210> 76
<211> 762
<212> DNA
<213> Secale cereale
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[illegible]

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<210> 77
<211> 254
<212> PRT
<213> Secale cereale
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<400> 77															
Val	Arg	Lys	Glu	Val	Val	Lys	Leu	Leu	Glu	Ala	Gly	Ile	Ile	Tyr	Pro
1				5					10					15	
Val	Ala	Asp	Ser	Gln	Trp	Val	Ser	His	Val	His	Tyr	Val	Pro	Lys	Lys
			20					25					30		
Gly	Gly	Met	Thr	Val	Val	Pro	Asn	Asp	Lys	Asp	Glu	Leu	Ile	Pro	Gln
		35					40					45			
Arg	Ile	Val	Thr	Gly	Tyr	Arg	Met	Val	Ser	Asp	Phe	Arg	Lys	Leu	Asn
	50					55					60				
Lys	Ala	Thr	Lys	Lys	Asp	His	Tyr	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met
65					70					75					80
Leu	Glu	Arg	Leu	Ser	Lys	His	Thr	His	Phe	Phe	Phe	Leu	Asp	Gly	Tyr

				85						90					95				
Ser	Gly	Phe	Ser	Gln	Ile	Pro	Val	Ser	Lys	Gly	Asp	Gln	Glu	Lys	Thr				
			100					105					110						
Thr	Phe	Thr	Cys	Thr	Phe	Gly	Thr	Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe				
		115					120					125							
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Met	Ala	Ile				
		130				135					140								
Phe	Ser	Asp	Phe	Cys	Glu	Lys	Ile	Val	Glu	Val	Phe	Met	Asp	Asp	Phe				
145				150					155					160					
Ser	Val	Tyr	Gly	Thr	Ser	Phe	Asp	Asp	Cys	Leu	Ser	Asn	Leu	Asp	Arg				
			165				170						175						
Val	Leu	Gln	Arg	Cys	Glu	Asp	Thr	Asn	Leu	Val	Leu	Asn	Cys	Glu	Lys				
		180					185						190						
Cys	His	Phe	Met	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Ile	Ser				
		195					200					205							
Glu	Ile	Gly	Ile	Glu	Val	Asp	Lys	Ala	Lys	Val	Asp	Ala	Ile	Glu	Lys				
		210				215					220								
Met	Pro	Cys	Ala	Lys	Asp	Ile	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His				
225				230					235					240					
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Ser	Lys	Val						
			245				250												

<210> 78

<211> 759

<212> DNA

<213> Secale cereale

<400> 78

gtgcgcaagg	aagtttttaa	gtttctagag	gcaggtataa	tctatccagt	tgctgatagc	60
cagtgggtaa	gtcctgtcca	ttgtgtccct	aagaagggag	gtatgactgt	agttccta	120
gataaagatg	aattgatctc	gcaaagaatt	gttacaggtt	ataggatggt	aattgatttt	180
cgcaaattaa	ataaagccac	taagaaagat	caataccctt	tgccctttat	tgatcaaatg	240
ctagaaagggt	tatccaaaca	caccattttt	tgctttctag	atgggtattc	tagtttctct	300
caaataccta	tgtcaaaagg	ggataaagaa	aagaccactt	ttacttgtcc	ctttgggtact	360
ttgcttatag	acgtatgcct	tttggtttat	gtaatgcac	tgctaccttt	caaacatgca	420
tgatggctat	actctatgat	ttttgtgaaa	gaatgttgat	gttttcatgg	atgatttttg	480
tatttacgaa	acttcttttg	atgattgctt	gagcaacctt	gatcgagttt	tgcaagatg	540
tgaagaaact	aatcttgtct	tgaactggga	aaagtccac	tttatgggta	atgaaggcat	600
tgcttgggac	ataaaatttc	tgaagagggt	accgaagttg	acaaagctaa	agttgatgct	660
gttgaaaaga	tgccatgtcc	caaggacatc	aaaggtataa	gaagtttcct	tggtcatgcc	720
gggttttata	ggaggtttat	caaggacttc	accaaggtt			759

<210> 79

<211> 254

<212> PRT

<213> Secale cereale

<400> 79

Val	Arg	Lys	Glu	Val	Phe	Lys	Phe	Leu	Glu	Ala	Gly	Ile	Ile	Tyr	Pro
1				5				10						15	
Val	Ala	Asp	Ser	Gln	Trp	Val	Ser	Pro	Val	His	Cys	Val	Pro	Lys	Lys
			20				25					30			
Gly	Gly	Met	Thr	Val	Val	Pro	Asn	Asp	Lys	Asp	Glu	Leu	Ile	Ser	Gln
		35				40					45				
Arg	Ile	Val	Thr	Gly	Tyr	Arg	Met	Val	Ile	Asp	Phe	Arg	Lys	Leu	Asn
	50				55				60						
Lys	Ala	Thr	Lys	Lys	Asp	Gln	Tyr	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met

65					70					75					80
Leu	Glu	Arg	Leu	Ser	Lys	His	Thr	His	Phe	Cys	Phe	Leu	Asp	Gly	Tyr
				85					90					95	
Ser	Ser	Phe	Ser	Gln	Ile	Pro	Met	Ser	Lys	Gly	Asp	Lys	Glu	Lys	Thr
			100					105					110		
Thr	Phe	Thr	Cys	Pro	Phe	Gly	Thr	Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe
		115					120					125			
Gly	Leu	Cys	Asn	Ala	Ser	Ala	Thr	Phe	Gln	Thr	Cys	Met	Met	Ala	Ile
	130					135					140				
Leu	Tyr	Asp	Phe	Cys	Glu	Arg	Ile	Val	Asp	Val	Phe	Met	Asp	Asp	Phe
145					150				155					160	
Cys	Ile	Tyr	Glu	Thr	Ser	Phe	Asp	Asp	Cys	Leu	Ser	Asn	Leu	Asp	Arg
				165					170					175	
Val	Leu	Gln	Arg	Cys	Glu	Glu	Thr	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys
			180					185					190		
Ser	His	Phe	Met	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Ile	Ser
		195					200					205			
Glu	Arg	Gly	Thr	Glu	Val	Asp	Lys	Ala	Lys	Val	Asp	Ala	Val	Glu	Lys
	210					215					220				
Met	Pro	Cys	Pro	Lys	Asp	Ile	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His
225				230						235					240
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
				245					250						

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<210> 80
<211> 761
<212> DNA
<213> Triticum aestivum
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<400>	80						
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cagtgggtaa	gtcctgtcca	ttgtgtccct	aagaaggag	gtattactgt	tgtcccta		120
gataaagatg	aattgattcc	tcaaagaatt	attacggtta	taggatggta	attgatttcc		180
gcaaattaaa	taaagccact	aagagagatc	attacccctt	acctttttatt	gatcaaattc		240
tagaaagatt	atgcaaacat	acacattatt	gcttccaaga	tggttatcct	ggtttttctc		300
aaatacctgt	gtcggctaaa	gatcaatcaa	agactacttt	tacatgccct	tttggtactt		360
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tgatggctat	attctctgat	ttttgtgaaa	agattttgta	ggttttcatg	gatgactttt		480
ccgtctatgg	ttcctctttt	gatgattgct	tgagcaatct	tgatcgagtt	ttgcagagat		540
gtgaagaaac	taactctgtc	ttgaattggg	aaaagtgtca	ctttatgggt	aatgaaggta		600
ttgtcttggg	gcacaaagtt	tctgaaagag	gtattgaagt	tgataaagcc	aagggttgaca		660
ctattgaaaa	gataccatgt	cccaaggaca	tcaaaggta	aagaagtttc	cttggtcacg		720
ccgqattttta	taggaggttc	ataaaaagatt	tcacaaaggt	t			761

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<210> 81
<211> 254
<212> PRT
<213> Triticum aestivum
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<400> 81															
Val	Arg	Lys	Glu	Val	Leu	Lys	Phe	Leu	Glu	Val	Gly	Ile	Ile	Tyr	Pro
1				5					10					15	
Val	Ala	Asp	Ser	Gln	Trp	Val	Ser	Pro	Val	His	Cys	Val	Pro	Lys	Lys
			20					25					30		
Gly	Gly	Ile	Thr	Val	Val	Pro	Asn	Asp	Lys	Asp	Glu	Leu	Ile	Pro	Gln
		35					40					45			
Arg	Ile	Ile	Thr	Gly	Tyr	Arg	Met	Val	Ile	Asp	Phe	Arg	Lys	Leu	Asn

50		55		60
Lys Ala Thr Lys Arg Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Ile				
65		70		75
Leu Glu Arg Leu Cys Lys His Thr His Tyr Cys Phe Gln Asp Gly Tyr				80
	85		90	95
Pro Gly Phe Ser Gln Ile Pro Val Ser Ala Lys Asp Gln Ser Lys Thr				
	100		105	110
Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Cys Met Pro Phe				
	115		120	125
Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile				
	130		135	140
Phe Ser Asp Phe Cys Glu Lys Ile Cys Glu Val Phe Met Asp Asp Phe				
145		150		155
Ser Val Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg				160
	165		170	175
Val Leu Gln Arg Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys				
	180		185	190
Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser				
	195		200	205
Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Thr Ile Glu Lys				
	210		215	220
Ile Pro Cys Pro Lys Asp Ile Lys Gly Thr Arg Ser Phe Leu Gly His				
225		230		235
Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val				240
	245		250	

<210> 82

<211> 780

<212> DNA

<213> Triticum aestivum

<400> 82

gtgcggaagg	aggtgttttaa	gctccttgag	gcagggtataa	tttatcccgt	tgctgatagt	60
aagtgggtaa	ttcctgtcca	tttaagtgatc	gtgattactg	ttgttcctaa	gaagggaggt	120
attaccgttg	ttcctaata	taaagatgaa	ttgattcctc	aaagaaccat	tactggttat	180
aggatggtaa	ttgatttccg	caaattaaat	aaggctacta	aaaaatatca	ttacccttta	240
ccttttatcg	atcaaagtct	agaaagatta	tccaaacata	cacatttttg	ctttctagat	300
ggttactctg	gtttctctca	aatacctgtg	tcagccaaag	atcaatcaaa	gactactttt	360
acatgccctt	ttggtacttt	tgcttataga	cgtatgcctt	ttgggtttatg	taatgcacct	420
gctacctttc	aaagatacat	gatggctata	ttatctgact	tttgtgaaaa	gatttgtgag	480
gttttcatgg	acgactcttc	catctatgga	tcttcttttg	atgattgctt	gagcaacctt	540
gatcgagttt	tgcaagatg	tgaagaaact	tatcttgtct	tgaattggga	aaagtgccaa	600
tttatggtta	atgaaggtat	tgtcctgggg	cataaagttt	ctgaaagagg	tattcgagtt	660
gataaagcca	aggttgatgc	tattgaaaag	atgccatgtc	ccatggacat	caaaggtata	720
agaagtttcc	ttggtcatgc	cggtttttat	aggaggttca	taaaagactt	cacgaaggtt	780

<210> 83

<211> 260

<212> PRT

<213> Triticum aestivum

<400> 83

Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Ile Ile Tyr Pro				
1	5		10	15
Val Ala Asp Ser Lys Trp Val Ile Pro Val His Glx Val Ile Val Ile				
	20		25	30
Thr Val Val Pro Lys Lys Gly Gly Ile Thr Val Val Pro Asn Asp Lys				

35	40	45
Asp Glu Leu Ile Pro Gln Arg Thr Ile Thr Gly Tyr Arg Met Val Ile		
50	55	60
Asp Phe Arg Lys Leu Asn Lys Ala Thr Lys Lys Tyr His Tyr Pro Leu		
65	70	75
Pro Phe Ile Asp Gln Met Leu Glu Arg Leu Ser Lys His Thr His Phe		
85	90	95
Cys Phe Leu Asp Gly Tyr Ser Gly Phe Ser Gln Ile Pro Val Ser Ala		
100	105	110
Lys Asp Gln Ser Lys Thr Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala		
115	120	125
Tyr Arg Arg Met Pro Phe Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln		
130	135	140
Arg Tyr Met Met Ala Ile Leu Ser Asp Phe Cys Glu Lys Ile Cys Glu		
145	150	155
Val Phe Met Asp Asp Ser Ser Ile Tyr Gly Ser Ser Phe Asp Asp Cys		
165	170	175
Leu Ser Asn Leu Asp Arg Val Leu Gln Arg Cys Glu Glu Thr Tyr Leu		
180	185	190
Val Leu Asn Trp Glu Lys Cys Gln Phe Met Val Asn Glu Gly Ile Val		
195	200	205
Leu Gly His Lys Val Ser Glu Arg Gly Ile Arg Val Asp Lys Ala Lys		
210	215	220
Val Asp Ala Ile Glu Lys Met Pro Cys Pro Met Asp Ile Lys Gly Ile		
225	230	235
Arg Ser Phe Leu Gly His Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp		
245	250	255
Phe Thr Lys Val		
260		

<210> 84

<211> 762

<212> DNA

<213> Triticum aestivum

<400> 84

gtgcgtaagg	aggtattcaa	gcttctggag	gcaggtataa	tttatcccgt	tgttgatagt	60
caatgggtaa	gtcctgtcca	ttgtgtcctt	aagaaggag	gtattactgt	tgtcccta	120
gataaagatg	aattgattcc	gcaaagaatt	atcacagggt	ataggatggg	aattgatttc	180
cgtaagttaa	ataaagctac	taagaaagat	cattaccctt	taccttttat	tgatcaaagt	240
ttagaaagat	tatgcaaaca	tacacattat	tgctttctag	atgggtattc	tgggtttctt	300
caaatacctg	tgtagctaa	ggatcaatca	aagactactt	ttacatgccc	ttttgggtact	360
tttggttata	gacgtatgcc	tttcgattta	tgtaatgcac	ctgctacctt	tcaaataatgc	420
atgatggcta	tattctctga	cttttgcgaa	aagattttgtg	agggttttcat	ggacgacttt	480
tccgtctatg	gttcctctta	tgatgattgc	ttgagcaatc	ttaatcgagt	tttgagagaga	540
tgtgaagaaa	ctaattctgt	cttgaattgg	gaaaagtgcc	actttatggg	taatgaagggt	600
attgtcttgg	ggcacaaagt	ttctgaacga	ggtattgaag	ttgataaggc	caagggttgat	660
gctattgaaa	agatgacatg	tcccaaggac	atcaaaggta	taagaagttt	ccttggtcac	720
gccagatttt	ataggaggtt	cataaaaagac	ttcacaagg	tt		762

<210> 85

<211> 254

<212> PRT

<213> Triticum aestivum

<400> 85

Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Ile Ile Tyr Pro

1	5	10	15
Val Val Asp	Ser Gln Trp Val Ser	Pro Val His Cys Val	Leu Lys Lys
	20	25	30
Gly Gly Ile	Thr Val Val Pro Asn Asp	Lys Asp Glu Leu Ile	Pro Gln
	35	40	45
Arg Ile Ile	Thr Gly Tyr Arg Met Val	Ile Asp Phe Arg Lys	Leu Asn
	50	55	60
Lys Ala Thr	Lys Lys Asp His Tyr Pro	Leu Pro Phe Ile Asp	Gln Met
65	70	75	80
Leu Glu Arg	Leu Cys Lys His Thr His	Tyr Cys Phe Leu Asp	Gly Tyr
	85	90	95
Ser Gly Phe	Ser Gln Ile Pro Val Ser	Ala Lys Asp Gln Ser	Lys Thr
	100	105	110
Thr Phe Thr	Cys Pro Phe Gly Thr Phe	Gly Tyr Arg Arg Met	Pro Phe
	115	120	125
Asp Leu Cys	Asn Ala Pro Ala Thr Phe	Gln Ile Cys Met Met	Ala Ile
	130	135	140
Phe Ser Asp	Phe Cys Glu Lys Ile Cys	Glu Val Phe Met Asp	Asp Phe
145	150	155	160
Ser Val Tyr	Gly Ser Ser Tyr Asp Asp	Cys Leu Ser Asn Leu	Asn Arg
	165	170	175
Val Leu Gln	Arg Cys Glu Glu Thr Asn	Leu Val Leu Asn Trp	Glu Lys
	180	185	190
Cys His Phe	Met Val Asn Glu Gly Ile Val	Leu Gly His Lys Val	Ser
	195	200	205
Glu Arg Gly	Ile Glu Val Asp Lys Ala Lys	Val Asp Ala Ile Glu	Lys
	210	215	220
Met Thr Cys	Pro Lys Asp Ile Lys Gly Ile	Arg Ser Phe Leu Gly	His
225	230	235	240
Ala Arg Phe	Tyr Arg Arg Phe Ile Lys Asp	Phe Thr Lys Val	
	245	250	

<210> 86

<211> 762

<212> DNA

<213> Triticum aestivum

<400> 86

gtgcggaaag	agggtgctcaa	gcttctggag	gcagggtataa	tttatcccgt	tgctgagagt	60
cagtgggtaa	gtcctgtcca	ttgtgtccct	aagaaggagg	gtattactgt	tgccctaata	120
gataaagatg	aattgattcc	tcaaagaatt	attacagggt	ataggatggg	aattgatttc	180
cgcaaattaa	ataaagccac	caagaaagat	cattaccctt	taccttttat	tgatcaaata	240
ctagaaagat	tatgcaaaca	tacacattat	tgcttcctag	atggttatct	tggtttctct	300
caaatacctg	tgtcggctaa	agatcaatca	aagactactt	ttacatgccc	ttttggtact	360
tttgcttata	gacgtatgcc	ttttggttta	tgtaatgcac	cttctacctt	tcaaagatgc	420
atgatggcta	tattctctga	tttttgtgaa	aagatttgtg	aggttttcat	ggacgaattt	480
tccgtctatg	gttcctcttt	tgatgattgc	ttgagcaatc	ctgatcgagt	tttgcagaga	540
tgtgaagaaa	ctaattctgt	cttgaattgg	gaaaagtgcc	actttatggt	taatgaagg	600
attgtcttgg	ggcacaaaag	ttctgaaaga	ggtattgaa	ttgataaagc	caaggttgac	660
gctattgaaa	agatgccatg	tcccaaggac	atcaaaggta	taagaagttt	ccttggtcac	720
gccggatttt	ataggagggt	cataaaagac	ttcacaaagg	tt		762

<210> 87

<211> 254

<212> PRT

<213> Triticum aestivum

<400> 87

Val Arg Lys Glu Val Leu Lys Leu Leu Glu Ala Gly Ile Ile Tyr Pro
 1 5 10 15
 Val Ala Glu Ser Gln Trp Val Ser Pro Val His Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln
 35 40 45
 Arg Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn
 50 55 60
 Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Cys Lys His Thr His Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Phe Ser Gln Ile Pro Val Ser Ala Lys Asp Gln Ser Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ser Thr Phe Gln Arg Cys Met Met Ala Ile
 130 135 140
 Phe Ser Asp Phe Cys Glu Lys Ile Cys Glu Val Phe Met Asp Glu Phe
 145 150 155 160
 Ser Val Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Pro Asp Arg
 165 170 175
 Val Leu Gln Arg Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205
 Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys
 210 215 220
 Met Pro Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 88

<211> 762

<212> DNA

<213> Triticum aestivum

<400> 88

gtgcgtaagg aggttttcaa gttccttgag gcagggtatta cttatcccgt tgctgatagt 60
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 gataaagatg aattgatccc gcaaataatt attacagggt ataggatggg aattgatttc 180
 cataagttaa ataaagctac taagaaagat cattaccctt tacctcttat tgatcaaatt 240
 ctagaaagac tatccaaaca cacacatttc tgctttctag atgggtatac tggtttctct 300
 caaataacctg tgtcagtga ggatcaatct aaaactactt ttacttgccc ttttggtact 360
 tttgcttata gacttatgcc ttttggttta tgtaatgcac ctacttcctt tcaaagatgc 420
 atgatggcta tattctctgt tttttgtgaa aatatttgtg aggtattcat ggatgatttc 480
 tccgtttatg gacccctctt tgatgattgt ttgagcaacc ttgatcgagt tttgcagaga 540
 tgcgaagaca ctagtctcat cctgaattgg gaaaagtgtc actttatggg taatgaaggc 600
 attgtcttgg ggcataagat ttccgagaga ggtattgaag ttgacaaagc caaagttgat 660
 gctattgaaa agattccatg tcccaaggac ataaaaggta taagaagttt ccttggtcat 720
 gctgggtttt ataggagggt catcaaagac ttctcaaagg tt 762

<210> 89

<211> 254

<212> PRT

<213> Triticum aestivum

<400> 89

Val Arg Lys Glu Val Phe Lys Phe Leu Glu Ala Gly Ile Thr Tyr Pro
 1 5 10 15
 Val Ala Asp Ser Glu Trp Val Ser Pro Leu His Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Ile Thr Val Val Leu Asn Asp Lys Asp Glu Leu Ile Pro Gln
 35 40 45
 Ile Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe His Lys Leu Asn
 50 55 60
 Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Leu Ile Asp Gln Ile
 65 70 75 80
 Leu Glu Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asp Gly Tyr
 85 90 95
 Thr Gly Phe Ser Gln Ile Pro Val Ser Val Lys Asp Gln Ser Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Leu Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Thr Ser Phe Gln Arg Cys Met Met Ala Ile
 130 135 140
 Phe Ser Val Phe Cys Glu Asn Ile Cys Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg
 165 170 175
 Val Leu Gln Arg Cys Glu Asp Thr Ser Leu Ile Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser
 195 200 205
 Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys
 210 215 220
 Ile Pro Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Ser Lys Val
 245 250

<210> 90

<211> 791

<212> DNA

<213> Gossypium hirsutum

<400> 90

gtgcgcaagg aggtttttaa gctacttgat gacgggatga tctatcccat atctaacagt 60
 aattgggtta gccagtaga catagtagca aaaaagacca gtgcaaccgt aatcgagaat 120
 tcggcagggtg agatagttcc cactcgggtc caaaacgggt ggagagtatg catcgattac 180
 aggaagtga attccttaac tcggaaggat cactttccac ttctttttat tgaccagatg 240
 ttagaacgtt tagctggaaa gtctcattat ttagaacgtt tagctggaaa gtctcattat 300
 tgttgtttgg atggttacta aggttttttc cagatcccag tggcaccgga ggatcaagaa 360
 agacaatgtt tacgtgcca tttggcacgt tttcttacag acggatgccg ttcggactct 420
 gtaatgcacc agccagtttt cataggtgca tggtaagtat attttcagac tacgtcgata 480
 aaattatcga ggtgttcacg gacgacttta ctgtatatgg tgagtccttc gaggttaagtc 540
 tgacgaacct tgcaaaaatt ttggaaaagat gcttagaatt taatcttggt ctaaattatg 600
 agaaaatgcca ttttatggta gacaagggat tagttctagg tcatattatt tctgctgatg 660
 gaatttctgt tgataaagca aaaatcaaca tcattaactc actaccatac cccacaactg 720
 tgaggagat ttggtctttc cttggtcatg caggtttcta caagtgggtc atcaaagact 780
 tttcaaaagt t 791

<210> 91
 <211> 264
 <212> PRT
 <213> Gossypium hirsutum

<400> 91
 Val Arg Lys Glu Val Leu Lys Leu Leu Asp Asp Gly Met Ile Tyr Pro
 1 5 10 15
 Ile Ser Asn Ser Asn Trp Val Ser Pro Val His Ile Val Pro Lys Lys
 20 25 30
 Thr Ser Ala Thr Val Ile Glu Asn Ser Ala Gly Glu Ile Val Pro Thr
 35 40 45
 Arg Val Gln Asn Gly Trp Arg Val Cys Ile Asp Tyr Arg Lys Leu Asn
 50 55 60
 Ser Leu Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ala Gly Lys Ser His Tyr Leu Glu Arg Leu Ala Gly
 85 90 95
 Lys Ser His Tyr Cys Cys Leu Asp Gly Tyr Glx Gly Phe Phe Gln Ile
 100 105 110
 Pro Val Ala Pro Glu Asp Gln Glu Lys Thr Met Phe Thr Cys Pro Phe
 115 120 125
 Gly Thr Phe Ser Tyr Arg Arg Met Pro Phe Gly Leu Cys Asn Ala Pro
 130 135 140
 Ala Ser Phe His Arg Cys Met Val Ser Ile Phe Ser Asp Tyr Val Asp
 145 150 155 160
 Lys Ile Ile Glu Val Phe Met Asp Asp Phe Thr Val Tyr Gly Glu Ser
 165 170 175
 Phe Glu Val Ser Leu Thr Asn Leu Ala Lys Ile Leu Glu Arg Cys Leu
 180 185 190
 Glu Phe Asn Leu Val Leu Asn Tyr Glu Lys Cys His Phe Met Val Asp
 195 200 205
 Lys Gly Leu Val Leu Gly His Ile Ile Ser Ala Asp Gly Ile Ser Val
 210 215 220
 Asp Lys Ala Lys Ile Asn Ile Ile Asn Ser Leu Pro Tyr Pro Thr Thr
 225 230 235 240
 Val Arg Glu Ile Trp Ser Phe Leu Gly His Ala Gly Phe Tyr Lys Trp
 245 250 255
 Phe Ile Lys Asp Phe Ser Lys Val
 260

<210> 92
 <211> 763
 <212> DNA
 <213> Gossypium hirsutum

<400> 92
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 aattgggtta gtccagtcca catagtaccc aaaaagaccg gtgtaaccgt aattgagaat 120
 tcagcaggtg agatggttcc cacttaagtc cgaaacggtc ggagagtatg catcgattac 180
 aggaagttga attccttaac tcggaaagat cactttccac ttctttttat tgatcagatg 240
 ttagaacatt tagccagaaa gtctcattat tgttgctctg atgggttactc aggttttttc 300
 cagatcccaa tggcactaaa ggatcaagaa aagatgacat ttacgtgccc atttggcattg 360
 ttcgcttata gaaggatgtc gtttcagact ttgcaatgca ccaaccatgt ttcagagggtg 420
 catgataagt atattttttg actatgttaa gaaaataatt gaggtgttca tggacgaatt 480
 tactgtatat agtgagtcct tcgaggtata tttgtcaa atctagaaaaat ttttggaag 540
 atgccttagaa ttttaatttg ttctaaatta tgagaattgc tatttaattgg tagacaaggg 600

attagttcta ggtcatatca tttctgctaa gggaatttct gtcgataaag taaaaattaa 660
 catcataagc tcaataccat accccacaac tgtgaggag attcgttctt tccttagtca 720
 tataggtttc tataggcgat tcatcaagga cttttcaaaa gtt 763

<210> 93

<211> 254

<212> PRT

<213> Gossypium hirsutum

<400> 93

Val	Arg	Lys	Glu	Val	Val	Lys	Leu	Leu	Asp	Ser	Gly	Met	Ile	Tyr	Pro
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Ile	Ser	Asp	Asn	Asn	Trp	Val	Ser	Pro	Val	His	Ile	Val	Pro	Lys	Lys
		20					25					30			
Thr	Gly	Val	Thr	Val	Ile	Glu	Asn	Ser	Ala	Gly	Glu	Met	Val	Pro	Thr
	35					40					45				
Glx	Val	Arg	Asn	Gly	Arg	Arg	Val	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn
50					55					60					
Ser	Leu	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Leu	Phe	Ile	Asp	Gln	Met
65					70				75					80	
Leu	Glu	His	Leu	Ala	Arg	Lys	Ser	His	Tyr	Cys	Cys	Leu	Asp	Gly	Tyr
		85						90					95		
Ser	Gly	Phe	Phe	Gln	Ile	Pro	Met	Ala	Leu	Lys	Asp	Gln	Glu	Lys	Met
		100						105				110			
Thr	Phe	Thr	Cys	Pro	Phe	Gly	Met	Phe	Ala	Tyr	Arg	Arg	Met	Ser	Phe
	115					120					125				
Arg	Leu	Cys	Asn	Ala	Pro	Thr	Met	Phe	Gln	Arg	Cys	Met	Ile	Ser	Ile
130						135					140				
Phe	Phe	Asp	Tyr	Val	Lys	Lys	Ile	Ile	Glu	Val	Phe	Met	Asp	Glu	Phe
145					150				155					160	
Thr	Val	Tyr	Ser	Glu	Ser	Phe	Glu	Val	Tyr	Leu	Ser	Asn	Leu	Glu	Lys
		165						170					175		
Phe	Leu	Glu	Arg	Cys	Leu	Glu	Phe	Asn	Leu	Val	Leu	Asn	Tyr	Glu	Asn
	180							185				190			
Cys	Tyr	Leu	Met	Val	Asp	Lys	Gly	Leu	Val	Leu	Gly	His	Ile	Ile	Ser
	195						200					205			
Ala	Lys	Gly	Ile	Ser	Val	Asp	Lys	Val	Lys	Ile	Asn	Ile	Ile	Ser	Ser
	210					215					220				
Ile	Pro	Tyr	Pro	Thr	Thr	Val	Arg	Glu	Ile	Arg	Ser	Phe	Leu	Ser	His
225					230				235					240	
Ile	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Ser	Lys	Val		
			245					250							

<210> 94

<211> 723

<212> DNA

<213> Gossypium hirsutum

<400> 94

gtgcgtaagg	aggttttgaa	attgttgat	gctggaatga	tatactcgat	ctttgacagt	60
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tcatcaggag	agctagtccc	taccgagtc	cagaatcgat	ggagggttg	catcgattac	180
aggaagtga	acgcagctac	ccgaaatgac	cattttccac	ttcccttcat	tgatcaaatg	240
ctcgagcgat	tagctaataa	gaccattat	tgttgtctcg	atgggtactc	aggacttttc	300
caaattccgg	tggcacctga	ggatcaagac	aaaacaactt	tcacgtgccc	ctttggaacg	360
tttgcgtata	gaagaatgtc	gtttggactc	tgtaatgtc	cggccacttt	ccagagatgt	420
atggtgagca	tattctctga	ttatgtcgag	aaaatcattg	aattcttcat	ggatgacttc	480

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acgggtgtacg gtaactcttt taacgaatgt ctcgataatc ttgctaagat attacagaga      540
tgcctagaat ttaatcttgt tttaaattat gaaaaatgcc acttcatggg tgacaaagga      600
ttaattttgg gtcatatagt ttcttcagaa ggtattgagg tcaataaagc aaaaacgaat      660
attattgact cattacctta ccccgattt tacagacgat tcataaagga cttcacaaaa      720
gtt                                                                    723

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<210> 95

<211> 241

<212> PRT

<213> *Gossypium hirsutum*

<400> 95

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Val Arg Lys Glu Val Leu Lys Leu Leu Asp Ala Gly Met Ile Tyr Ser
1          5          10          15
Ile Phe Asp Ser Asp Trp Val Ser Trp Val His Val Val Pro Lys Lys
20          25          30
Thr Gly Val Thr Val Val Lys Asn Ser Ser Gly Glu Leu Val Pro Thr
35          40          45
Arg Val Gln Asn Arg Trp Arg Val Cys Ile Asp Tyr Arg Lys Leu Asn
50          55          60
Ala Ala Thr Arg Asn Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met
65          70          75          80
Leu Glu Arg Leu Ala Asn Lys Thr His Tyr Cys Cys Leu Asp Gly Tyr
85          90          95
Ser Gly Leu Phe Gln Ile Pro Val Ala Pro Glu Asp Gln Asp Lys Thr
100         105         110
Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Ser Phe
115         120         125
Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Val Ser Ile
130         135         140
Phe Ser Asp Tyr Val Glu Lys Ile Ile Glu Phe Phe Met Asp Asp Phe
145         150         155         160
Thr Val Tyr Gly Asn Ser Phe Asn Glu Cys Leu Asp Asn Leu Ala Lys
165         170         175
Ile Leu Gln Arg Cys Leu Glu Phe Asn Leu Val Leu Asn Tyr Glu Lys
180         185         190
Cys His Phe Met Val Asp Lys Gly Leu Ile Leu Gly His Ile Val Ser
195         200         205
Ser Glu Gly Ile Glu Val Asn Lys Ala Lys Thr Asn Ile Ile Asp Ser
210         215         220
Leu Pro Tyr Pro Arg Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys
225         230         235         240
Val

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<210> 96

<211> 762

<212> DNA

<213> *Lycopersicon esculentum*

<400> 96

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gaaaaaaatg agttgatccc aaccatgata gtcacataat ggagaatatg catggattac      180
aggaaattga atgaagccac caggaaggac cattaccggg tcccttttat tgatcagatg      240
ttggaccggg tggctgggga ataattattat tgttttctta atggctattt acggtacaac      300
caaattgtga tttcaccaaa ggattaagag aaaaccactt tcacttgccc gtatggtaca      360

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tatgctttca	aaaagatacc	ttttgggtta	tgaaatgcct	cggtactttt	ccaatgatgc	420
atgatggcta	tttttcatga	tatggttgaa	gattttgttg	agatattcat	gaatgatttc	480
tcagtgtttg	gggattcttt	tgatatgtgc	ttggagaatt	tggacagtgt	gttggctagt	540
tgtgaagaaa	ctaattcttt	cctaaactgg	gaataatagc	aatttctagt	aaaggaaggg	600
attatgctag	gacataaggt	gtcaaagaga	ggtatggaag	ttgatagtgc	caaagtggag	660
gttattgaaa	agcttcccc	tcctatatct	gttaaaggga	tgcaaagttt	tctgggtcat	720
gttgggttct	ataggagatt	cataaaagac	ttcacaaagg	tt		762

<210> 97

<211> 254

<212> PRT

<213> *Lycopersicon esculentum*

<400> 97

Val	Arg	Lys	Glu	Val	Val	Lys	Leu	Leu	Asp	Thr	Gly	Ile	Val	Glx	Pro
1				5					10					15	
Ile	Ser	Asp	Asn	Lys	Glx	Val	Ser	Pro	Val	Gln	Cys	Glu	Pro	Lys	Lys
			20					25					30		
Gly	Asp	Ile	Thr	Val	Ile	Thr	Asn	Glu	Lys	Asn	Glu	Leu	Ile	Pro	Thr
		35					40					45			
Met	Ile	Val	Thr	Glx	Trp	Arg	Ile	Cys	Met	Asp	Tyr	Arg	Lys	Leu	Asn
	50					55				60					
Glu	Ala	Thr	Arg	Lys	Asp	His	Tyr	Pro	Val	Pro	Phe	Ile	Asp	Gln	Met
65					70					75				80	
Leu	Asp	Arg	Leu	Ala	Gly	Glu	Glx	Tyr	Tyr	Cys	Phe	Leu	Asn	Gly	Tyr
			85					90					95		
Leu	Arg	Tyr	Asn	Gln	Ile	Val	Ile	Ser	Pro	Lys	Asp	Glx	Glu	Lys	Thr
			100					105					110		
Thr	Phe	Thr	Cys	Pro	Tyr	Gly	Thr	Tyr	Ala	Phe	Lys	Lys	Ile	Pro	Phe
	115					120						125			
Gly	Leu	Glx	Asn	Ala	Ser	Ala	Thr	Phe	Gln	Glx	Cys	Met	Met	Ala	Ile
	130				135						140				
Phe	His	Asp	Met	Val	Glu	Asp	Phe	Val	Glu	Ile	Phe	Met	Asn	Asp	Phe
145					150					155				160	
Ser	Val	Phe	Gly	Asp	Ser	Phe	Asp	Met	Cys	Leu	Glu	Asn	Leu	Asp	Ser
			165					170					175		
Val	Leu	Ala	Ser	Cys	Glu	Glu	Thr	Asn	Leu	Phe	Leu	Asn	Trp	Glu	Glx
		180						185					190		
Glx	Gln	Phe	Leu	Val	Lys	Glu	Gly	Ile	Met	Leu	Gly	His	Lys	Val	Ser
	195						200					205			
Lys	Arg	Gly	Met	Glu	Val	Asp	Ser	Ala	Lys	Val	Glu	Val	Ile	Glu	Lys
	210					215					220				
Leu	Pro	Pro	Pro	Ile	Ser	Val	Lys	Gly	Met	Gln	Ser	Phe	Leu	Gly	His
225					230					235				240	
Val	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
			245					250							

<210> 98

<211> 689

<212> DNA

<213> *Lycopersicon esculentum*

<400> 98

cgaaaggagg	tggtgaaact	ggaaattatc	aagtagttgg	atgctagagt	aatctatcca	60
atcgccgata	gtagttgggt	atgcctagtt	cagtgtgtac	caaagaaagg	gggaatgact	120
gtgggtcccca	acgaaaagaa	tgaacttggt	cgaatgagac	cggttactgg	atggagggtg	180
tgcattggatt	accgtaaact	gaactcatag	actgaaaaag	actattttca	tatgcccttc	240

atggatcaga	tggttgatag	acttgccgga	aaaggggtggt	attgttttct	tgatgggtat	300
tcgggggtata	atcagatttc	tattgcacca	gaagatcaag	agaaaaccac	tttcacttgt	360
ccatacggga	cttttgcat	cagaagaatg	tcgtttgggt	tgtgcaatgc	acccgcaacc	420
tttcagagat	ggatgatgtc	aatattttct	gacatgatgg	aggatactat	agagggtttt	480
atggatgatt	tttctgtggt	tggtgattca	ttcgagcggt	gcttgtccaa	tttatctgag	540
gttcttaaga	gatgtgaaga	ctgcaatttg	gtactaaact	gggaaaagtg	tcatttcatg	600
gtgaaagagg	gtattgtgtt	gggtcatcgc	atttcagaaa	agggcatgca	tgtttttact	660
ggtgattcat	caaagacttc	acaaagggt				689

<210> 99

<211> 229

<212> PRT

<213> Lycopersicon esculentum

<400> 99

Arg	Lys	Glu	Val	Val	Lys	Leu	Glu	Ile	Ile	Lys	Glx	Leu	Asp	Ala	Arg
1				5					10					15	
Val	Ile	Tyr	Pro	Ile	Ala	Asp	Ser	Ser	Trp	Val	Cys	Leu	Val	Gln	Cys
			20					25					30		
Val	Pro	Lys	Lys	Gly	Gly	Met	Thr	Val	Val	Pro	Asn	Glu	Lys	Asn	Glu
		35					40					45			
Leu	Val	Arg	Met	Arg	Pro	Val	Thr	Gly	Trp	Arg	Val	Cys	Met	Asp	Tyr
	50					55					60				
Arg	Lys	Leu	Asn	Ser	Glx	Thr	Glu	Lys	Asp	Tyr	Phe	His	Met	Pro	Phe
65					70					75					80
Met	Asp	Gln	Met	Leu	Asp	Arg	Leu	Ala	Gly	Lys	Gly	Trp	Tyr	Cys	Phe
			85						90					95	
Leu	Asp	Gly	Tyr	Ser	Gly	Tyr	Asn	Gln	Ile	Ser	Ile	Ala	Pro	Glu	Asp
		100						105					110		
Gln	Glu	Lys	Thr	Thr	Phe	Thr	Cys	Pro	Tyr	Gly	Thr	Phe	Ala	Phe	Arg
	115						120					125			
Arg	Met	Ser	Phe	Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Trp
	130					135					140				
Met	Met	Ser	Ile	Phe	Ser	Asp	Met	Met	Glu	Asp	Thr	Ile	Glu	Val	Phe
145					150					155					160
Met	Asp	Asp	Phe	Ser	Val	Val	Gly	Asp	Ser	Phe	Glu	Arg	Cys	Leu	Ser
			165					170						175	
Asn	Leu	Ser	Glu	Val	Leu	Lys	Arg	Cys	Glu	Asp	Cys	Asn	Leu	Val	Leu
		180						185					190		
Asn	Trp	Glu	Lys	Cys	His	Phe	Met	Val	Lys	Glu	Gly	Ile	Val	Leu	Gly
	195						200					205			
His	Arg	Ile	Ser	Glu	Lys	Gly	Met	His	Val	Phe	Thr	Gly	Asp	Ser	Ser
	210					215					220				
Lys	Thr	Ser	Gln	Arg											
225															

<210> 100

<211> 760

<212> DNA

<213> Lycopersicon esculentum

<400> 100

gtgcgtaagg	aggtgtttta	gcttctagat	gcgggtattg	tctacccaat	taggacaaca	60
agtggggttag	tctagtacaa	tgtgtacct	aaaaggagg	catggcaatg	attactaatg	120
aaaacaatga	gtttatccca	accagcacag	tcacaagatg	gcgaatatgc	atgaattaca	180
cgaagttaat	gaagccacta	ggaagaatca	ttacccaatt	ctttttattg	attatatgtt	240
ggaccgggta	gctgggcaag	aatattattg	ttttttggat	tactaatcag	ggtacaacta	300

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aatttttgatt gcaccagagg atcaagagaa aacaactttc acttgcccgt atggtacata 360
tgcttttcaag aggatacctt ttgggttatg caatgctctg tctaatttcc aaagatgcat 420
gatgactatt tttcatgata tgggtgaata ttttgaggat atattcatgg atgatttctt 480
agtgttttgg gagtcttttg atagatgctt ggagaatttg aacaggttgt tagctagggtg 540
cgaacaaact aatcttgtcc tgaactggga aaaatgtcat tttttagtaa aggaagggaa 600
tttttcgggg cataaggtgt aaaagatagg gctggaagtt gatcatgaca aagtgggaagt 660
aattgaaaag atctcctctc ccatttttgt gaaacgggtg agaagtttac taggtcatgc 720
tgagttttac aggatattca tcaaggactt ctcaaaggtt 760

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<210> 101
 <211> 254
 <212> PRT
 <213> *Lycopersicon esculentum*

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<400> 101
Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Ile Val Tyr Pro
1 5 10 15
Ile Ser Asp Asn Lys Trp Val Ser Leu Val Gln Cys Val Pro Lys Lys
20 25 30
Gly Gly Met Ala Met Ile Thr Asn Glu Asn Asn Glu Phe Ile Pro Thr
35 40 45
Ser Thr Val Thr Arg Trp Arg Ile Cys Met Asn Tyr Thr Lys Leu Asn
50 55 60
Glu Ala Thr Arg Lys Asn His Tyr Pro Ile Leu Phe Ile Asp Tyr Met
65 70 75 80
Leu Asp Arg Leu Ala Gly Gln Glu Tyr Tyr Cys Phe Leu Asp Tyr Glx
85 90 95
Ser Gly Tyr Asn Glx Ile Leu Ile Ala Pro Glu Asp Gln Glu Lys Thr
100 105 110
Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Phe Lys Arg Ile Pro Phe
115 120 125
Gly Leu Cys Asn Ala Leu Ser Asn Phe Gln Arg Cys Met Met Thr Ile
130 135 140
Phe His Asp Met Val Glu Tyr Phe Glu Asp Ile Phe Met Asp Asp Phe
145 150 155 160
Leu Val Phe Trp Glu Ser Phe Asp Arg Cys Leu Glu Asn Leu Asn Arg
165 170 175
Leu Leu Ala Arg Cys Glu Gln Thr Asn Leu Val Leu Asn Trp Glu Lys
180 185 190
Cys His Phe Leu Val Lys Glu Gly Asn Phe Ser Gly His Lys Val Glx
195 200 205
Lys Ile Gly Leu Glu Val Asp His Asp Lys Val Glu Val Ile Glu Lys
210 215 220
Ile Ser Ser Pro Ile Phe Val Lys Arg Val Arg Ser Leu Leu Gly His
225 230 235 240
Ala Glu Phe Tyr Arg Ile Phe Ile Lys Asp Phe Ser Lys Val
245 250

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<210> 102
 <211> 776
 <212> DNA
 <213> *Lycopersicon esculentum*

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<400> 102
gtgcggaaag aagtgtttaa actggaatca ttaaattggtt ggatgctgga gtaatatatc 60
cgatctccga tagtagttgg gtatgcccta ttcagtgtgt acctaaagaaa ggggggaatga 120
ctgtggtccc caataagaaa aatgaacttg ttctaagtag accggttact ggaggggtggg 180

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tgtgtatgga	ttaccgtaaa	ttaaattgcat	ggactgaaaa	agaccattttt	cctatgccct	240
tcatggatca	gatgttggat	agacttgccg	aaaaaggggtg	gtactgtttt	cttcatggat	300
agtcagggtg	taattagatt	tctattgcac	cagaagatca	agagaaaacc	acattttactt	360
gtccatatgg	gacctttgca	ttgaagagaa	tgtcgtttgg	gttgtgcaat	gcacccgcca	420
cattttcacag	atgtaaaaaat	gttgatattc	ttcgacatgg	tggatgatac	tattgatgct	480
tttatggatg	atttttctct	tgttggtgaa	tcattcgaga	ggtgtttgaa	ccatttatct	540
gatgtcctta	agagatgtga	agactgcaat	ttagtactaa	attgggaaaa	atgccacttc	600
atggtgaaaa	aaggtattgt	tttgggtcat	cgcattccag	aaaagggcat	agaggttgat	660
cgagctaaag	tagaggtaat	agagagactt	ccccactat	ctctgtaaaa	ggtgtgagaa	720
gctttcttgg	gcatgcaagt	ttttaccgga	gattcatcaa	agacttcaca	aaagtt	776

<210> 103

<211> 258

<212> PRT

<213> *Lycopersicon esculentum*

<400> 103

Ala	Glu	Arg	Ser	Val	Glx	Thr	Gly	Ile	Ile	Lys	Trp	Leu	Asp	Ala	Gly
1				5					10					15	
Val	Ile	Tyr	Pro	Ile	Ser	Asp	Ser	Ser	Trp	Val	Cys	Pro	Ile	Gln	Cys
			20					25					30		
Val	Pro	Lys	Lys	Gly	Gly	Met	Thr	Val	Val	Pro	Asn	Lys	Lys	Asn	Glu
		35					40					45			
Leu	Val	Leu	Met	Arg	Pro	Val	Thr	Gly	Gly	Trp	Val	Cys	Met	Asp	Tyr
	50					55					60				
Arg	Lys	Leu	Asn	Ala	Trp	Thr	Glu	Lys	Asp	His	Phe	Pro	Met	Pro	Phe
65					70				75					80	
Met	Asp	Gln	Met	Leu	Asp	Arg	Leu	Ala	Glu	Lys	Gly	Trp	Tyr	Cys	Phe
			85					90						95	
Leu	Asp	Gly	Glx	Ser	Gly	Tyr	Asn	Glx	Ile	Ser	Ile	Ala	Pro	Glu	Asp
		100						105					110		
Gln	Glu	Lys	Thr	Thr	Phe	Thr	Cys	Pro	Tyr	Gly	Thr	Phe	Ala	Leu	Lys
	115						120					125			
Arg	Met	Ser	Phe	Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	His	Arg	Cys
	130					135					140				
Lys	Met	Leu	Ile	Phe	Phe	Asp	Met	Val	Asp	Asp	Thr	Ile	Asp	Ala	Phe
145					150				155					160	
Met	Asp	Asp	Phe	Ser	Leu	Val	Gly	Glu	Ser	Phe	Glu	Arg	Cys	Leu	Asn
			165					170						175	
His	Leu	Ser	Asp	Val	Leu	Lys	Arg	Cys	Glu	Asp	Cys	Asn	Leu	Val	Leu
	180							185					190		
Asn	Trp	Glu	Lys	Cys	His	Phe	Met	Val	Lys	Lys	Gly	Ile	Val	Leu	Gly
	195						200					205			
His	Arg	Ile	Pro	Glu	Lys	Gly	Ile	Glu	Val	Asp	Arg	Ala	Lys	Val	Glu
	210					215				220					
Val	Ile	Glu	Arg	Leu	Pro	Pro	Pro	Ile	Ser	Val	Lys	Gly	Val	Arg	Ser
225					230					235				240	
Phe	Leu	Gly	His	Ala	Ser	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr
			245					250						255	

Lys Val

<210> 104

<211> 761

<212> DNA

<213> *Solanum tuberosum*

<400> 104

gtgcggaagg	aggtacttaa	attgttggat	gcacggattg	tgtacccaat	atcagacagt	60
aaatgggtaa	gtccagtaaa	gtgtgtgccc	aagaagggca	gaatgacggt	gttgactaat	120
gagaagaatg	aggtaatccc	cacaagaaca	gtgactgggt	gacggatttg	catggactac	180
atgaagttga	acgacgccac	cagaaaggac	cattatccgg	tacctttcat	tgataaaata	240
ttggataggt	tggcaggaca	tgagtactat	tggtttcttg	gtgtctactc	agggtacaat	300
cagattgtta	ttgcaataga	ggactaggtg	aaaaccacct	tcacctgttc	gtatggcaca	360
tatgcgttca	agcacatgcc	attcggcttg	tgcaatgccc	tggccacatt	tcagagatgc	420
atgttggcaa	tcttccatga	tatggtggag	gattttgttg	aagttttcat	ggatgacttc	480
ttggtgtttg	gtgagtcttt	tgaactttgt	ttgactaatt	ttgacagatt	tcttgctagg	540
tgtgaagaga	cgaatctggt	gataaactga	tagaagtgtc	actttctggt	tcgagagggg	600
attgtgttgg	gacacaagat	ctccaaaaat	gggctgaaag	ttgacaaagc	caacgtagag	660
gttattgaga	aattgccacc	cccatcacag	tgaaggtaat	taaaagctta	ctaggacatg	720
cttggtttta	tacgaggttc	atcaaagact	tcacaaaggt	t		761

<210> 105

<211> 254

<212> PRT

<213> Solanum tuberosum

<400> 105

Val	Arg	Lys	Glu	Val	Leu	Lys	Leu	Leu	Asp	Ala	Arg	Ile	Val	Tyr	Pro
1				5					10					15	
Ile	Ser	Asp	Ser	Lys	Trp	Val	Ser	Pro	Val	Lys	Cys	Val	Pro	Lys	Lys
			20					25					30		
Gly	Arg	Met	Thr	Val	Leu	Thr	Asn	Glu	Lys	Asn	Glu	Val	Ile	Pro	Thr
			35				40					45			
Arg	Thr	Val	Thr	Gly	Glx	Arg	Ile	Cys	Met	Asp	Tyr	Met	Lys	Leu	Asn
	50					55					60				
Asp	Ala	Thr	Arg	Lys	Asp	His	Tyr	Pro	Val	Pro	Phe	Ile	Asp	Lys	Ile
65				70					75					80	
Leu	Asp	Arg	Leu	Ala	Gly	His	Glu	Tyr	Tyr	Cys	Phe	Leu	Gly	Val	Tyr
			85					90					95		
Ser	Gly	Tyr	Asn	Gln	Ile	Val	Ile	Ala	Ile	Glu	Asp	Glx	Val	Lys	Thr
			100					105					110		
Thr	Phe	Thr	Cys	Ser	Tyr	Gly	Thr	Tyr	Ala	Phe	Lys	His	Met	Pro	Phe
		115					120					125			
Gly	Leu	Cys	Asn	Ala	Leu	Ala	Thr	Phe	Gln	Arg	Cys	Met	Leu	Ala	Ile
	130					135					140				
Phe	His	Asp	Met	Val	Glu	Asp	Phe	Val	Glu	Val	Phe	Met	Asp	Asp	Phe
145				150					155					160	
Leu	Val	Phe	Gly	Glu	Ser	Phe	Glu	Leu	Cys	Leu	Thr	Asn	Phe	Asp	Arg
			165					170					175		
Phe	Leu	Ala	Arg	Cys	Glu	Glu	Thr	Asn	Leu	Val	Ile	Asn	Glx	Glx	Lys
		180						185				190			
Cys	His	Phe	Leu	Val	Arg	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Ile	Ser
	195					200					205				
Lys	Asn	Gly	Leu	Lys	Val	Asp	Lys	Ala	Asn	Val	Glu	Val	Ile	Glu	Lys
	210				215						220				
Leu	Pro	Pro	Pro	Ile	Thr	Val	Lys	Val	Ile	Lys	Ser	Leu	Leu	Gly	His
225				230					235					240	
Ala	Trp	Phe	Tyr	Thr	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
			245					250							

<210> 106

<211> 760

<212> DNA

<213> Solanum tuberosum

<400> 106

gtgcgtaaag	agggttttcaa	actgctagat	gtcgggtattg	tatatccgat	ttcagaaagc	60
aaatgggtca	gcccagttta	gtgtgtgcct	aaaaaaagag	gcatgccggt	gatcaccaat	120
gaaaaaaatg	agttgattcc	aaccaggaca	gtgacagggt	ggcgaatatg	catggattat	180
aggaaattga	atgaggccac	cagaaaggat	cactgcccgg	ttccttttat	tgatcagatg	240
ctggacaggt	tagttgggca	agaatattat	tgtttcctgg	aaggctattc	aggatacaac	300
caaattgtga	ttgcaccaga	ggaccaggag	aaaactacat	tcacttgtct	gtatggggaca	360
tatgctttca	agtgactgcc	gtttggggcta	tgcaatgctc	cagccacctt	ccaaagatga	420
atgatggcta	tctttcatga	tatggttgaa	gattttgtgg	agatattcat	ggatgacttc	480
tcagtcttta	gggagtcttt	tgataggtgt	ttggagaatt	gggacagggt	gctggctaga	540
tgcgaggaaa	ctaattctcat	cctaaactgg	aaaaaatgtc	atttcctagt	aaatgaaggg	600
attgtattgg	gccataaggt	gtcaaagaga	gggctggaag	ttgatcgtgc	caaagtggaa	660
gttattgaaa	aactacctcc	tccaatctgt	taaaggggtg	agaagctttc	tgggtcatgc	720
tggtttttac	aggagattta	taaaggactt	cacaaaggtt			760

<210> 107

<211> 254

<212> PRT

<213> Solanum tuberosum

<400> 107

Val	Arg	Lys	Glu	Val	Phe	Lys	Leu	Leu	Asp	Val	Gly	Ile	Val	Tyr	Pro
1				5				10						15	
Ile	Ser	Glu	Ser	Lys	Trp	Val	Ser	Pro	Val	Glx	Cys	Val	Pro	Lys	Lys
		20						25					30		
Arg	Gly	Met	Pro	Val	Ile	Thr	Asn	Glu	Lys	Asn	Glu	Leu	Ile	Pro	Thr
		35					40					45			
Arg	Thr	Val	Thr	Gly	Trp	Arg	Ile	Cys	Met	Asp	Tyr	Arg	Lys	Leu	Asn
	50					55					60				
Glu	Ala	Thr	Arg	Lys	Asp	His	Cys	Pro	Val	Pro	Phe	Ile	Asp	Gln	Met
65					70				75						80
Leu	Asp	Arg	Leu	Val	Gly	Gln	Glu	Tyr	Tyr	Cys	Phe	Leu	Glu	Gly	Tyr
				85				90					95		
Ser	Gly	Tyr	Asn	Gln	Ile	Val	Ile	Ala	Pro	Glu	Asp	Gln	Glu	Lys	Thr
			100					105					110		
Thr	Phe	Thr	Cys	Leu	Tyr	Gly	Thr	Tyr	Ala	Phe	Lys	Glx	Leu	Pro	Phe
		115					120					125			
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Glx	Met	Met	Ala	Ile
	130					135					140				
Phe	His	Asp	Met	Val	Glu	Asp	Phe	Val	Glu	Ile	Phe	Met	Asp	Asp	Phe
145					150				155						160
Ser	Val	Phe	Arg	Glu	Ser	Phe	Asp	Arg	Cys	Leu	Glu	Asn	Trp	Asp	Arg
			165					170					175		
Val	Leu	Ala	Arg	Cys	Glu	Glu	Thr	Asn	Leu	Ile	Leu	Asn	Trp	Lys	Lys
		180						185					190		
Cys	His	Phe	Leu	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Val	Ser
		195					200					205			
Lys	Arg	Gly	Leu	Glu	Val	Asp	Arg	Ala	Lys	Val	Glu	Val	Ile	Glu	Lys
	210					215					220				
Leu	Pro	Pro	Pro	Ile	Ser	Val	Lys	Gly	Val	Arg	Ser	Phe	Leu	Gly	His
225					230					235					240
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
				245					250						

<210> 108

<211> 761
 <212> DNA
 <213> Solanum tuberosum

<400> 108
 gtgcgtaaag aggttttcaa gctctggatg caggtattgt ctatccaatt tcagacagca 60
 agtgggtcag tccagttcag tgtgtgccta aaaagggagg catgacgggtg atcactaatg 120
 aaaaaaatga gttgattcca accaggacag tgacaggatg gcgaatatgc atggattaca 180
 gaaaattaaa tgaagctacc agaaaggatc actaccgggt tccttttatt gatcagatgc 240
 tggacagggtt ggctggacaa gaatattatt gtttcttgga tggttattca ggatacaacc 300
 aaatagtgat tgcaccagag gaccagggga aaactacatt cacttgcttg tatgggacat 360
 atgtttccaa gagaatgtcg tttgggctat gcaatgctcc atccattttc caaagatgca 420
 tgatggccat cttccatgat aaggttgaag attttatgga aatattcatg gatgacttct 480
 cagtatttgg ggagtctttt gacagggtgct tggagaattt agacagagtg ttggctagat 540
 gcgaggaaac taattttgtc ctaaactggg aaaaatgtca tttcctagtg aaggaaggga 600
 ttgtgttggg tcataaggtg tcaaagagag ggctggaagt tgatcgtgcc agagtggaaa 660
 taatcaaaaa gctacctccc ccaatttctg ttaaaggggt gcgaagtttt ttgggtcatg 720
 ttagtttcta cgaaagattc ataaaggact tcaccaaggt t 761

<210> 109
 <211> 254
 <212> PRT
 <213> Solanum tuberosum

<400> 109
 Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Ile Val Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Lys Trp Val Ser Pro Val Gln Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Ile Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr
 35 40 45
 Arg Thr Val Thr Gly Trp Arg Ile Cys Met Asp Tyr Arg Lys Leu Asn
 50 55 60
 Glu Ala Thr Arg Lys Asp His Tyr Pro Val Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Asp Arg Leu Ala Gly Gln Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Val Ile Ala Pro Glu Asp Gln Gly Lys Thr
 100 105 110
 Thr Phe Thr Cys Leu Tyr Gly Thr Tyr Val Ser Lys Arg Met Ser Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ser Ile Phe Gln Arg Cys Met Met Ala Ile
 130 135 140
 Phe His Asp Lys Val Glu Asp Phe Met Glu Ile Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Phe Gly Glu Ser Phe Asp Arg Cys Leu Glu Asn Leu Asp Arg
 165 170 175
 Val Leu Ala Arg Cys Glu Glu Thr Asn Phe Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Leu Val Lys Glu Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205
 Lys Arg Gly Leu Glu Val Asp Arg Ala Arg Val Glu Ile Ile Lys Lys
 210 215 220
 Leu Pro Pro Pro Ile Ser Val Lys Gly Val Arg Ser Phe Leu Gly His
 225 230 235 240
 Val Ser Phe Tyr Glu Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 110
 <211> 762
 <212> DNA
 <213> Solanum tuberosum

<400> 110
 gtgcgtaagg aggtcctcaa gctgtctgat gcaggaattg tgtaccccat ttatgatata 60
 aagtggatca gcccagttca ctgtgtgccg aaaaagggag gcatgacgat tattactaat 120
 gaaaagaagg agttgatttc agctagaacg gtgatagagt ggcacatatg aatggactat 180
 aggagactaa atgaggcaac tagaaaggaa cactacccag ttccctttcat tgatcaaatg 240
 ttggacaggt ttattgggca agagtattat tgtttcctag atggctattc aggatataat 300
 caaattgtga ttgcgccata agataaagag aaaactacat ttacttctct atatgggaca 360
 tatgccttca agagaatgtc gtttgggccg tgcaatgtc caaccacatt ccaaagatgc 420
 atgacagcca tttttcatga tatggtcaaa tattttgtgg agatattcat ggatgaattc 480
 ttagtctttg gggagtcttt tgacacgtgt ctagaatatt tggacaatgt gcttgccaga 540
 tgtgaggaaa ctaatcccggt cctcaactgg gaaaaatgtc attttctagt gaagaagggg 600
 attgtactag gccacaagggt ttcagaggaa ggactggaag ttgatcgtgg aaaagtagag 660
 gtaatttaaa agctaccccc tcaagtcttc gttaaagggg tgagaagggt ccttggtcat 720
 tctaggttcg aaatgagatt cataaaagac ttcacaaaag tt 762

<210> 111
 <211> 254
 <212> PRT
 <213> Solanum tuberosum

<400> 111
 Val Arg Lys Glu Val Leu Lys Leu Ser Asp Ala Gly Ile Val Tyr Pro
 1 5 10 15
 Ile Tyr Asp Ile Lys Trp Ile Ser Pro Val His Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Ile Ile Thr Asn Glu Lys Lys Glu Leu Ile Ser Ala
 35 40 45
 Arg Thr Val Ile Glu Trp His Ile Glx Met Asp Tyr Arg Arg Leu Asn
 50 55 60
 Glu Ala Thr Arg Lys Glu His Tyr Pro Val Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Asp Arg Phe Ile Gly Gln Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Val Ile Ala Pro Glx Asp Lys Glu Lys Thr
 100 105 110
 Thr Phe Thr Ser Leu Tyr Gly Thr Tyr Ala Phe Lys Arg Met Ser Phe
 115 120 125
 Gly Pro Cys Asn Ala Pro Thr Thr Phe Gln Arg Cys Met Thr Ala Ile
 130 135 140
 Phe His Asp Met Val Lys Tyr Phe Val Glu Ile Phe Met Asp Glu Phe
 145 150 155 160
 Leu Val Phe Gly Glu Ser Phe Asp Thr Cys Leu Glu Tyr Leu Asp Asn
 165 170 175
 Val Leu Ala Arg Cys Glu Glu Thr Asn Pro Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Leu Val Lys Lys Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205
 Glu Glu Gly Leu Glu Val Asp Arg Gly Lys Val Glu Val Ile Glx Lys
 210 215 220
 Leu Pro Pro Gln Val Phe Val Lys Gly Val Arg Arg Phe Leu Gly His
 225 230 235 240

Ser Arg Phe Glu Met Arg Phe Ile Lys Asp Phe Thr Lys Val
245 250

<210> 112
<211> 762
<212> DNA
<213> Solanum tuberosum

<400> 112
gtgcggaagg aggttttttaa gctgctggat gcggggtattg tataccagat ttcagatagc 60
aaaggggtct acccgattta gtttgtgcct aaaaaatgca gcatgacagt gatcaccaat 120
gaaaagaatg agctgattcc aaccaggaca gtgacagggt ggccaatatg catggattat 180
atgaagttga atgaggccac cagaaaggat cactaccga ttcattttat tgatcagatg 240
ttggacaagt tagctgagta aaaatattat tgtttcttgg cttgttattc aagatacaac 300
caattttctca ttgcaccaca ggaccaggag gaaactacat tcacttgtcc ttatgggaca 360
tatgcttttca agcgaatgtc gtttgggcta tgcaatgctc caaccacctt ccaaagatgc 420
ataagggcta tctttcatga tatggttgaa gattttgtgg agatattcat ggatgacttc 480
tcagtctttg ggtagtcttt tgagagggtg ctggaaaatt ttgacagggt gctggctgta 540
tgcgaggaaa ctaatttttt cctaaactgg gaaaaatgtc attttctagt gaaggaaggg 600
attgtattgg gacataaggt gtcaaagtga aggcttgaag ttgatcgtgc caaagtggaa 660
gtcgttgaaa acctaccttc cccattctct gttaaagggg tgagaagttt tttgggtcat 720
gctggtttct ataggagatt tatcaaagac ttcactaagg tt 762

<210> 113
<211> 254
<212> PRT
<213> Solanum tuberosum

<400> 113
Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Ile Val Tyr Gln
1 5 10 15
Ile Ser Asp Ser Lys Gly Val Tyr Pro Ile Glx Phe Val Pro Lys Lys
20 25 30
Cys Ser Met Thr Val Ile Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr
35 40 45
Arg Thr Val Thr Gly Trp Arg Ile Cys Met Asp Tyr Met Lys Leu Asn
50 55 60
Glu Ala Thr Arg Lys Asp His Tyr Pro Ile His Phe Ile Asp Gln Met
65 70 75 80
Leu Asp Lys Leu Ala Glu Glx Lys Tyr Tyr Cys Phe Leu Ala Cys Tyr
85 90 95
Ser Arg Tyr Asn Gln Phe Leu Ile Ala Pro Gln Asp Gln Glu Glu Thr
100 105 110
Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Phe Lys Arg Met Ser Phe
115 120 125
Gly Leu Cys Asn Ala Pro Thr Phe Gln Arg Cys Ile Arg Ala Ile
130 135 140
Phe His Asp Met Val Glu Asp Phe Val Glu Ile Phe Met Asp Asp Phe
145 150 155 160
Ser Val Phe Gly Glx Ser Phe Glu Arg Cys Leu Glu Asn Phe Asp Arg
165 170 175
Val Leu Ala Val Cys Glu Glu Thr Asn Phe Phe Leu Asn Trp Glu Lys
180 185 190
Cys His Phe Leu Val Lys Glu Gly Ile Val Leu Gly His Lys Val Ser
195 200 205
Lys Glx Arg Leu Glu Val Asp Arg Ala Lys Val Glu Val Val Glu Asn
210 215 220

Leu Pro Ser Pro Phe Ser Val Lys Gly Val Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 114
 <211> 793
 <212> DNA
 <213> Solanum tuberosum

<400> 114
 aacttttgtg aagtcttttaa tgaaggatgt tgtcagagaa gaagtcatca agtggctgga 60
 tacagggatt gtgtacccaa tatctgacaa taaatgggca agtccagtgc agtgtgtgcc 120
 taaaaagggg ggaatgacag ttgtgaccaa tgagaaaaat gagttgatcc ccacaagaac 180
 agtaactggg tggaggctat gcatggacta cagaaaactc aatgaagcca ccaggaagga 240
 ccactattcg gtaccgttca ttgatcaaat gttagacagg ttggctggcc aagagtatta 300
 ctgtttcctt gatggttatt caaggtataa ttagatcgtc attgcacctg aggatcaaga 360
 gaatacgaca ttcacttgcc catatggcac gtatgcattc aaacgcttgc cattcggtt 420
 gtgcaatgcc ccaaccctat ttcagagatg tatgatggca atcttccatg atatggtgga 480
 agattttgtt aaagtataca tggacgattt ctcggtgttt ggtgagtcgt tcgaactttg 540
 tttatctaata cgtgatagag ttcttactag gtgtgaggag accaatttgg tgctgaactg 600
 ggagaagtgt cactttcttg ttagagaagg aattatgttg gggcagaaga tctccaaaag 660
 tgggctagaa gtagacaagg cgaaggtgga agtgattgag aagttgccac caccaatata 720
 agtaaagggg gtgcgaagct tccttggaca tgctgggttt tacaagaggt tcataaagga 780
 cttttcaag gtt 793

<210> 115
 <211> 264
 <212> PRT
 <213> Solanum tuberosum

<400> 115
 Thr Phe Val Lys Ser Leu Met Lys Asp Val Val Arg Glu Glu Val Ile
 1 5 10 15
 Lys Trp Leu Asp Thr Gly Ile Val Tyr Pro Ile Ser Asp Asn Lys Trp
 20 25 30
 Ala Ser Pro Val Gln Cys Val Pro Lys Lys Gly Gly Met Thr Val Val
 35 40 45
 Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr Arg Thr Val Thr Gly Trp
 50 55 60
 Arg Leu Cys Met Asp Tyr Arg Lys Leu Asn Glu Ala Thr Arg Lys Asp
 65 70 75 80
 His Tyr Ser Val Pro Phe Ile Asp Gln Met Leu Asp Arg Leu Ala Gly
 85 90 95
 Gln Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr Ser Arg Tyr Asn Glx Ile
 100 105 110
 Val Ile Ala Pro Glu Asp Gln Glu Asn Thr Thr Phe Thr Cys Pro Tyr
 115 120 125
 Gly Thr Tyr Ala Phe Lys Arg Leu Pro Phe Gly Leu Cys Asn Ala Pro
 130 135 140
 Thr Leu Phe Gln Arg Cys Met Met Ala Ile Phe His Asp Met Val Glu
 145 150 155 160
 Asp Phe Val Lys Val Tyr Met Asp Asp Phe Ser Val Phe Gly Glu Ser
 165 170 175
 Phe Glu Leu Cys Leu Ser Asn Arg Asp Arg Val Leu Thr Arg Cys Glu
 180 185 190
 Glu Thr Asn Leu Val Leu Asn Trp Glu Lys Cys His Phe Leu Val Arg

195					200					205					
Glu	Gly	Ile	Met	Leu	Gly	Gln	Lys	Ile	Ser	Lys	Ser	Gly	Leu	Glu	Val
210					215					220					
Asp	Lys	Ala	Lys	Val	Glu	Val	Ile	Glu	Lys	Leu	Pro	Pro	Pro	Ile	Glx
225					230					235					
Val	Lys	Gly	Val	Arg	Ser	Phe	Leu	Gly	His	Ala	Gly	Phe	Tyr	Lys	Arg
245					250					255					
Phe	Ile	Lys	Asp	Phe	Ser	Lys	Val								
260															

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<210> 116
<211> 761
<212> DNA
<213> Platanus occidentalis
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<400>	116						
gtgcgtaagg	aggttttcaa	acttcctaaa	gtttgagtga	tttatcctat	ttaggatagg		60
aattgggtca	gcccggttca	agtgggttcc	aaaaagattg	gaataaccgt	tgtgaaaaat		120
tagaatgatg	agttgggtcc	taccagtgtt	cagaatgggt	ggagggttgt	atagattata		180
gaaaattgaa	tgttgtaacc	cgcaaggatc	acttcacctt	acctttttatt	gatcaaattgc		240
ttgaaagggt	agttgggtcat	tcttactatt	gtttccctaga	tggttattca	agttattttcc		300
agattgtaat	tactccagag	gattaagaaa	agacaacctt	tacatgtcca	tttgggactt		360
ttgcatatcg	ttgcatgccc	tttggccctt	gcaatgcccc	aaccactttc	caaagggtga		420
tggttagcat	attttcatat	tacattgaga	atatcataga	agtttttatg	gatgatttca		480
tagtttatgg	agactccttt	aataattttc	tgcataacct	tacatttggt	cttcaaagat		540
gcatagaaac	taacctttgt	ttaaattatg	aaaaatgtca	ttttatgggt	gaacaaggta		600
tagttttggg	tcatgcttatt	tcatctaaag	gaattgaggt	agataaagct	aaagttgata		660
ttattcaatc	tttactttat	ctcattagta	tgcggaaggt	tcattccttt	cttggacatg		720
caggttttcta	ccqaagattc	attaaagact	ttacaaaggt	t			761

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<210> 117
<211> 254
<212> PRT
<213> Platanus occidentalis
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<400> 117															
Val	Arg	Lys	Glu	Val	Phe	Lys	Leu	Leu	Lys	Val	Glx	Val	Ile	Tyr	Pro
1				5					10					15	
Ile	Glx	Asp	Arg	Asn	Trp	Val	Ser	Pro	Val	Gln	Val	Val	Pro	Lys	Lys
			20					25					30		
Ile	Gly	Ile	Thr	Val	Val	Lys	Asn	Glx	Asn	Asp	Glu	Leu	Val	Pro	Thr
		35					40					45			
Ser	Val	Gln	Asn	Gly	Trp	Arg	Val	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn
	50					55					60				
Val	Val	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met
65					70					75				80	
Leu	Glu	Arg	Leu	Val	Gly	His	Ser	Tyr	Tyr	Cys	Phe	Leu	Asp	Gly	Tyr
				85					90					95	
Ser	Ser	Tyr	Phe	Gln	Ile	Val	Ile	Thr	Pro	Glu	Asp	Glx	Glu	Lys	Thr
			100					105					110		
Thr	Phe	Thr	Cys	Pro	Phe	Gly	Thr	Phe	Ala	Tyr	Arg	Cys	Met	Pro	Phe
		115					120					125			
Gly	Leu	Cys	Asn	Ala	Pro	Thr	Thr	Phe	Gln	Arg	Cys	Met	Val	Ser	Ile
	130					135					140				
Phe	Ser	Tyr	Tyr	Ile	Glu	Asn	Ile	Ile	Glu	Val	Phe	Met	Asp	Asp	Phe
145					150					155					160
Ile	Val	Tyr	Gly	Asp	Ser	Phe	Asn	Asn	Phe	Leu	His	Asn	Leu	Thr	Leu

				165					170					175	
Val	Leu	Gln	Arg	Cys	Ile	Glu	Thr	Asn	Leu	Val	Leu	Asn	Tyr	Glu	Lys
			180					185					190		
Cys	His	Phe	Met	Val	Glu	Gln	Gly	Ile	Val	Leu	Gly	His	Val	Ile	Ser
		195					200					205			
Ser	Lys	Gly	Ile	Glu	Val	Asp	Lys	Ala	Lys	Val	Asp	Ile	Ile	Gln	Ser
	210					215					220				
Leu	Pro	Tyr	Leu	Ile	Ser	Met	Arg	Lys	Val	His	Ser	Phe	Leu	Gly	His
225					230					235					240
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
				245					250						

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<210> 118
<211> 762
<212> DNA
<213> Platanus occidentalis
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<400>	118									
gtgcgtaagg	aagttttcaa	gcttcttgaa	gttggagtga	tttatcttat	ttcgaatagc					60
aattgggtta	gcccgattca	agtggctcct	aaaaagactg	gaataaccgt	tgtgaaaaat					120
cagaatgatg	agtttagttcc	tacccatggt	cagaatgggt	ggtagggtttg	tataaattat					180
agaaaattaa	atgtttataac	ctgcaaggat	cacttcccct	taccttttat	tgataaaatg					240
cttgaaagg	tagctgggtca	ttcttactat	tgtttccttg	atggttatatt	aggttatatt					300
caaattgcaa	ttacttcgga	ggatcaagaa	aagatgattt	ttaagtgcc	attcgggact					360
tttgcatatc	gtcacatgcc	ctttggcctt	tgcaatgcc	caaccacttt	ctaaagggtgt					420
atggtttagca	tattttcaga	ttacattgag	aatatcatag	aagctcttat	ggatgatttc					480
acagtttatg	gagactcctt	tgataattgt	ctgcataacc	ttacatttgt	tattcaaaaga					540
tgcatagaaa	ctaacctagt	gttaaattct	taaaaatgtc	attttatgg	tgaacaagg					600
atagttttgg	gtcatgttgt	ttcatctagg	ggaattgagg	tagataaaacc	taaagttgat					660
attattcaaa	cttttacctta	ttccactagt	gtgcgagaag	ttcgttcttt	tcttggacat					720
qtaggttttt	actgaagatt	cataaaaagac	ttcaciaaagg	tt						762

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<210> 119
<211> 254
<212> PRT
<213> Platanus occidentalis
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<400> 119															
Val	Arg	Lys	Glu	Val	Phe	Lys	Leu	Leu	Glu	Val	Gly	Val	Ile	Tyr	Leu
1				5					10					15	
Ile	Ser	Asn	Ser	Asn	Trp	Val	Ser	Pro	Val	Gln	Val	Ala	Pro	Lys	Lys
			20					25					30		
Thr	Gly	Ile	Thr	Val	Val	Lys	Asn	Gln	Asn	Asp	Glu	Leu	Val	Pro	Thr
			35				40					45			
His	Val	Gln	Asn	Gly	Trp	Trp	Val	Cys	Ile	Asn	Tyr	Arg	Lys	Leu	Asn
						55					60				
Val	Ile	Thr	Cys	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Lys	Met
65					70					75					80
Leu	Glu	Arg	Leu	Ala	Gly	His	Ser	Tyr	Tyr	Cys	Phe	Leu	Asp	Gly	Tyr
				85					90					95	
Leu	Gly	Tyr	Phe	Gln	Ile	Ala	Ile	Thr	Ser	Glu	Asp	Gln	Glu	Lys	Met
				100				105					110		
Ile	Phe	Lys	Cys	Pro	Phe	Gly	Thr	Phe	Ala	Tyr	Arg	His	Met	Pro	Phe
							120					125			
Gly	Leu	Cys	Asn	Ala	Pro	Thr	Thr	Phe	Glx	Arg	Cys	Met	Val	Ser	Ile
						135					140				
Phe	Ser	Asp	Tyr	Ile	Glu	Asn	Ile	Ile	Glu	Val	Phe	Met	Asp	Asp	Phe

145		150		155		160
Thr Val Tyr Gly Asp	Ser Phe Asp Asn Cys Leu His Asn Leu Thr Leu					
	165		170		175	
Val Ile Gln Arg Cys Ile Glu Thr Asn Leu Val Leu Asn Ser Glx Lys						
	180		185		190	
Cys His Phe Met Val Glu Gln Gly Ile Val Leu Gly His Val Val Ser						
	195		200		205	
Ser Arg Gly Ile Glu Val Asp Lys Pro Lys Val Asp Ile Ile Gln Thr						
	210		215		220	
Leu Pro Tyr Ser Thr Ser Val Arg Glu Val Arg Ser Phe Leu Gly His						
225		230		235		240
Val Gly Phe Tyr Glx Arg Phe Ile Lys Asp Phe Thr Lys Val						
	245		250			

<210> 120

<211> 759

<212> DNA

<213> Platanus occidentalis

<400> 120

gtgcggaag	agggttttaa	gcttttggat	gtagggatta	tatacccaat	tttttatagt	60
aattaggtaa	gtccactca	agtggaacca	agaattctgg	tgtgactgta	gttaaaaatg	120
caaatgatga	attgattcca	aatagactca	ctattgggtg	gcgtgtatgc	attaactata	180
agaagttgaa	ctcagtgact	aggaaggacc	atttcccttt	accattcatg	actaaatcct	240
agaaagggtg	gctggtcaca	aattttatta	tttccctatat	ggttattcta	gatataacta	300
aatagagatt	gcacctgagg	actaagaaaa	taccactttt	acatgtccat	ttggcacttt	360
tgcttatcga	aggatgtcat	ttggattatg	taatgctctt	gccacgttct	aaagatgcat	420
gttgagtata	tttagtgata	tggtagaaca	ttttcttgag	gtgtttatgg	attttttttg	480
tttttggtaa	ttcatttgat	gattgtttgc	ataatttgaa	aaaagtgtta	aatagatgtg	540
aaggaaaaaa	acatcatttt	gaattgagag	aagtgtcatt	tcatggcttc	taaaagaatt	600
gtacttggtc	acattgtctc	ctcccaagga	attaaagtgg	tcaaagccaa	aattgaattg	660
atagtcaatt	tgccatgccc	aaagactctt	aaagacattc	gatcttttct	aggtcatgca	720
ggatttaaca	aaaggttcat	caaagacttc	acgaaagtt			759

<210> 121

<211> 254

<212> PRT

<213> Platanus occidentalis

<400> 121

Val Arg Lys Glu Val Phe Lys Leu Leu Asp Val Gly Ile Ile Tyr Pro	
1	5 10 15
Ile Phe Tyr Ser Asn Glx Val Ser Pro Thr Gln Val Val Pro Lys Asn	
	20 25 30
Ser Gly Val Thr Val Val Lys Asn Ala Asn Asp Glu Leu Ile Pro Asn	
	35 40 45
Arg Leu Thr Ile Gly Trp Arg Val Cys Ile Asn Tyr Lys Lys Leu Asn	
	50 55 60
Ser Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Glx Ile	
65	70 75 80
Leu Glu Arg Val Ala Gly His Lys Phe Tyr Tyr Phe Leu Tyr Gly Tyr	
	85 90 95
Ser Arg Tyr Asn Glx Ile Glu Ile Ala Pro Glu Asp Glx Glu Asn Thr	
	100 105 110
Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Ser Phe	
	115 120 125
Gly Leu Cys Asn Ala Leu Ala Thr Phe Glx Arg Cys Met Leu Ser Ile	

130	135	140
Phe Ser Asp Met Val Glu His Phe Leu Glu Val Phe Met Asp Asp Phe		
145	150	155
Phe Val Phe Gly Asn Ser Phe Asp Asp Cys Leu His Asn Leu Lys Lys		160
	165	170
Val Leu Asn Arg Cys Glu Glu Lys Asn Ile Ile Leu Asn Glx Glu Lys		175
	180	185
Cys His Phe Met Val Ser Lys Arg Ile Val Leu Gly His Ile Val Ser		190
	195	200
Ser Gln Gly Ile Lys Val Val Lys Ala Lys Ile Glu Leu Ile Val Asn		205
	210	215
Leu Pro Ser Pro Lys Thr Leu Lys Asp Ile Arg Ser Phe Leu Gly His		220
225	230	235
Ala Gly Phe Asn Lys Arg Phe Ile Lys Asp Phe Thr Lys Val		240
	245	250

<210> 122
 <211> 761
 <212> DNA
 <213> Platanus occidentalis

<400> 122	
tgcgtaaaga ggtggtcaag cttcttgaag ttggagtgat ttatcctatt tcggatagca	60
attggggttag cccggttcaa gtggttccta aaaagactgg aataaccgtt gtgaaaaatc	120
aaaatgatga gttagtctcct acccgtgttc agaatgggtg gcaggtttgt atagattata	180
taaaattaaa tgttgtaacc cgcaaggatc acttcccttt accttttatt gatcaaagt	240
ttgaaagggt agctggtcat tcttactatt gtttccttga tggatattca tgttattttt	300
agattgcaat tactccagag gatcaagaaa agacgacttt tacgtgccca ttcgggactt	360
tttcatatcg ttgcatgccc tttggccttt gcaacgcccc agccactttc caaagggtga	420
tggttagcat attttcagat tacattgaga atatcataga agtctttatg gatgatttca	480
tagtttatga agactccttt gataattgtc tgcataacct tacacttggt ttttaaagat	540
gcatagaaac taaccttggt ttaaattttg aaaaatgtca tgttatgggt gaataaggta	600
tagttttggg tcatgttggt tcatctatgg gaattgaggt agataaagtt aaagttgata	660
ttattcaatc tttaccttat cccattagtg tgcaggaagt tcgttctttt cttggacatg	720
cgggttttta ccaaagattc attaaagact tcacgaaagt t	761

<210> 123
 <211> 253
 <212> PRT
 <213> Platanus occidentalis

<400> 123
Arg Lys Glu Val Val Lys Leu Leu Glu Val Gly Val Ile Tyr Pro Ile
1 5 10 15
Ser Asp Ser Asn Trp Val Ser Pro Val Gln Val Val Pro Lys Lys Thr
20 25 30
Gly Ile Thr Val Val Lys Asn Gln Asn Asp Glu Leu Val Pro Thr Arg
35 40 45
Val Gln Asn Gly Trp Gln Val Cys Ile Asp Tyr Ile Lys Leu Asn Val
50 55 60
Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met Phe
65 70 75 80
Glu Arg Leu Ala Gly His Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr Ser
85 90 95
Cys Tyr Phe Glx Ile Ala Ile Thr Pro Glu Asp Gln Glu Lys Thr Thr
100 105 110
Phe Thr Cys Pro Phe Gly Thr Phe Ser Tyr Arg Cys Met Pro Phe Gly

115 120 125
 Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Val Ser Ile Phe
 130 135 140
 Ser Asp Tyr Ile Glu Asn Ile Ile Glu Val Phe Met Asp Asp Phe Ile
 145 150 155 160
 Val Tyr Glu Asp Ser Phe Asp Asn Cys Leu His Asn Leu Thr Leu Val
 165 170 175
 Phe Glx Arg Cys Ile Glu Thr Asn Leu Val Leu Asn Phe Glu Lys Cys
 180 185 190
 His Val Met Val Glu Glx Gly Ile Val Leu Gly His Val Val Ser Ser
 195 200 205
 Met Gly Ile Glu Val Asp Lys Val Lys Val Asp Ile Ile Gln Ser Leu
 210 215 220
 Pro Tyr Pro Ile Ser Val Gln Glu Val Arg Ser Phe Leu Gly His Ala
 225 230 235 240
 Gly Phe Tyr Gln Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 124
 <211> 761
 <212> DNA
 <213> Sorghum bicolor

<400> 124
 gtgcgtaaaag aggtcttcaa gctctatcat gctgggatta tttatcctgt gccgcatagt 60
 gagtgggtta gccctgttca agtagtgcca aagaaaggag gaatgacggt cgtaggaat 120
 gagaagaatg aactcatccc tcaacgaatt gtcactgggt ggcgtatgtg tattgactat 180
 caaaaactca acacggctac aaagaaagat aactttccgt tacccttcat tgatgaaatg 240
 ttggaacggc ttgcaaacca ctctttcttc tgtttccttg atggttattc tggatatcac 300
 caaatcccaa tccaccacaga tgaccaagaa aagactacct ttacatgccc gtatggaact 360
 tatgcataac gacgaatgtc gttcggactg tgcaatgtc cagcttcttt ccaacgggtgc 420
 atgatgtcta ttttctcgga catgattgag aagatcatgg aggttttcat ggatgatttt 480
 accgtctatg gtaaaacctt cgatcattgt ttggagaatt tagatagagt cttgcagcga 540
 tgtgaagaaa agcacttaat cctgaactgg gagaaatgcc attttatggt tcaggaagga 600
 atagtgttag gacataaagt gtccgaacgt ggtatagagg tggacaaagc aaagattgaa 660
 gttattgaaa aacttccacc tcccacgaat gtgaaaggat ccgtagcttc ttgggacatg 720
 cagggttcta tagatgcttc ataaaagact tcacaaagggt t 761

<210> 125
 <211> 254
 <212> PRT
 <213> Sorghum bicolor

<400> 125
 Val Arg Lys Glu Val Phe Lys Leu Tyr His Ala Gly Ile Ile Tyr Pro
 1 5 10 15
 Val Pro His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Val Arg Asn Glu Lys Asn Glu Leu Ile Pro Gln
 35 40 45
 Arg Ile Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Gln Lys Leu Asn
 50 55 60
 Thr Ala Thr Lys Lys Asp Asn Phe Pro Leu Pro Phe Ile Asp Glu Met
 65 70 75 80
 Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr His Gln Ile Pro Ile His Pro Asp Asp Gln Glu Lys Thr

			100					105				110			
Thr	Phe	Thr	Cys	Pro	Tyr	Gly	Thr	Tyr	Ala	Glx	Arg	Arg	Met	Ser	Phe
		115					120				125				
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Ser	Phe	Gln	Arg	Cys	Met	Met	Ser	Ile
	130					135					140				
Phe	Ser	Asp	Met	Ile	Glu	Lys	Ile	Met	Glu	Val	Phe	Met	Asp	Asp	Phe
145					150					155					160
Thr	Val	Tyr	Gly	Lys	Thr	Phe	Asp	His	Cys	Leu	Glu	Asn	Leu	Asp	Arg
			165					170						175	
Val	Leu	Gln	Arg	Cys	Glu	Glu	Lys	His	Leu	Ile	Leu	Asn	Trp	Glu	Lys
		180						185					190		
Cys	His	Phe	Met	Val	Gln	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Val	Ser
	195						200				205				
Glu	Arg	Gly	Ile	Glu	Val	Asp	Lys	Ala	Lys	Ile	Glu	Val	Ile	Glu	Lys
	210					215					220				
Leu	Pro	Pro	Pro	Thr	Asn	Val	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His
225					230					235					240
Ala	Gly	Phe	Tyr	Arg	Cys	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
			245						250						

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<210> 126
<211> 762
<212> DNA
<213> Sorghum bicolor
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[illegible]

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<210> 127
<211> 254
<212> PRT
<213> Sorghum bicolor
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<400> 127															
Val	Arg	Lys	Glu	Val	Leu	Lys	Leu	Leu	His	Ala	Gly	Ile	Ile	Tyr	Pro
1				5					10					15	
Val	Pro	His	Ser	Glu	Trp	Val	Ser	Pro	Val	Gln	Val	Val	Pro	Lys	Lys
			20					25					30		
Gly	Gly	Met	Thr	Val	Ile	Ile	Asn	Glu	Lys	Asn	Glu	Leu	Ile	Pro	Gln
		35					40					45			
Arg	Thr	Val	Thr	Gly	Trp	Gln	Met	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn
	50					55					60				
Lys	Ala	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Glu	Met
65					70					75				80	
Leu	Glu	Arg	Leu	Ala	Asn	His	Ser	Phe	Phe	Cys	Phe	Leu	Asp	Gly	Tyr

				85				90					95		
Ser	Gly	Tyr	His	Gln	Ile	Pro	Ile	His	Pro	Asp	Asp	Gln	Ser	Lys	Thr
			100					105					110		
Thr	Phe	Thr	Cys	Pro	Tyr	Gly	Thr	Tyr	Ala	Tyr	Arg	Arg	Met	Ser	Phe
			115					120					125		
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Ser	Phe	Gln	Arg	Cys	Met	Met	Ser	Ile
			130					135					140		
Phe	Ser	Asp	Met	Ile	Glu	Glu	Ile	Met	Glu	Val	Phe	Met	Asp	Asp	Phe
145					150					155					160
Ser	Val	Tyr	Gly	Lys	Ala	Phe	Asp	Ser	Cys	Leu	Glu	Asn	Leu	Asp	Lys
				165					170					175	
Val	Leu	Gln	Ser	Cys	Glu	Glu	Lys	His	Leu	Ile	Leu	Asn	Trp	Glu	Lys
				180				185					190		
Cys	His	Phe	Met	Val	Arg	Glu	Gly	Ile	Val	Leu	Gly	His	Leu	Val	Ser
			195					200					205		
Glu	Arg	Gly	Ile	Glu	Val	Asp	Lys	Ala	Glu	Ile	Glu	Val	Ile	Glu	Gln
						215					220				
Leu	Pro	Pro	Pro	Val	Asn	Ile	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His
225					230					235					240
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
				245					250						

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<210> 128
<211> 762
<212> DNA
<213> Sorghum bicolor
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<400>	128						
gtgcggaagg	aagtcttaaa	gcttttacac	actaggatta	tttatctcgt	tcctcatagt		60
gagtgggtta	gcacggtaca	agttgtgcc	aagaaaggag	gaatgtcgg	tgtaggaat		120
gagaagaacg	aattcatccc	tcaacaaact	gtcactgggt	ggcgtatgtg	cattgactac		180
caaaaactca	acaaggccac	aaggaaagat	cacttcccgt	tacctttcat	tgatgaaatg		240
ttgtaatggc	ttacaaatca	ctcgttcttt	tgtttccttg	aagggtattc	cagatatcat		300
caaatcccg	tccaccacga	tgaccaaagt	aagactactt	tcacatgacc	ctatggaact		360
tacgcatacc	gacgaatgtc	gttcagggtta	tgtaatgctc	cagcttcttt	tcaacgggtgc		420
atgatgtcta	ttttttccaa	tatgattgag	aaaatcatgg	aggtattcac	ggatgatttt		480
accgtatatg	gcaaaacctt	tgatgattgt	ttagagaatt	tggacaaagt	cttacaattg		540
tgtgaaggaa	agcacttaat	cgtaaaactag	gagaaatgcc	attttatggt	ccgagaagga		600
atagtgcctag	ggcacaaggt	gtccgaacgt	gggatagagg	tggatagagc	caagattgaa		660
gttattgaaa	aacttccacc	tcccacaaat	gtgaaagaca	tccgcagttt	tcttggacat		720
gcagggttct	ataggcgctt	catcaaagat	ttcaccaagg	tt			762

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<210> 129
<211> 254
<212> PRT
<213> Sorghum bicolor
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<400> 129															
Val	Arg	Lys	Glu	Val	Leu	Lys	Leu	Leu	His	Thr	Arg	Ile	Ile	Tyr	Leu
1				5					10					15	
Val	Pro	His	Ser	Glu	Trp	Val	Ser	Thr	Val	Gln	Val	Val	Pro	Lys	Lys
			20					25					30		
Gly	Gly	Met	Ser	Val	Val	Arg	Asn	Glu	Lys	Asn	Glu	Phe	Ile	Pro	Gln
		35					40					45			
Gln	Thr	Val	Thr	Gly	Trp	Arg	Met	Cys	Ile	Asp	Tyr	Gln	Lys	Leu	Asn
	50					55				60					
Lys	Ala	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Glu	Met

65					70					75					80
Leu	Glx	Trp	Leu	Thr	Asn	His	Ser	Phe	Phe	Cys	Phe	Leu	Glu	Gly	Tyr
				85					90					95	
Ser	Arg	Tyr	His	Gln	Ile	Pro	Ile	His	His	Asp	Asp	Gln	Ser	Lys	Thr
			100					105				110			
Thr	Phe	Thr	Glx	Pro	Tyr	Gly	Thr	Tyr	Ala	Tyr	Arg	Arg	Met	Ser	Phe
		115					120					125			
Arg	Leu	Cys	Asn	Ala	Pro	Ala	Ser	Phe	Gln	Arg	Cys	Met	Met	Ser	Ile
	130					135					140				
Phe	Ser	Asn	Met	Ile	Glu	Lys	Ile	Met	Glu	Val	Phe	Thr	Asp	Asp	Phe
145					150				155						160
Thr	Val	Tyr	Gly	Lys	Thr	Phe	Asp	Asp	Cys	Leu	Glu	Asn	Leu	Asp	Lys
			165					170						175	
Val	Leu	Gln	Leu	Cys	Glu	Gly	Lys	His	Leu	Ile	Val	Asn	Glx	Glu	Lys
		180						185					190		
Cys	His	Phe	Met	Val	Arg	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Val	Ser
		195					200					205			
Glu	Arg	Gly	Ile	Glu	Val	Asp	Arg	Ala	Lys	Ile	Glu	Val	Ile	Glu	Lys
	210					215					220				
Leu	Pro	Pro	Pro	Thr	Asn	Val	Lys	Asp	Ile	Arg	Ser	Phe	Leu	Gly	His
225					230				235						240
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
				245					250						

<210> 130

<211> 761

<212> DNA

<213> Sorghum bicolor

<400> 130

gtg	cgtaagg	agg	tttttaa	gct	gctgcat	gcagagatta	tatatcatgt	gccgcacagt	60
gag	tgggtaa	gcc	cagttca	agt	tgtgcct	aaaaagggag	gcatgattgt	tgttacgaat	120
gaaaagaacg	agctaattcc	gca	acgcacc	gtc	acagggt	ggcggatgtg	catagactat		180
agaaaactaa	acaaagccac	gaga	aaggat	catt	ttcctt	tacctttcat	agatgagatg		240
ctagagcgat	tagcaaacca	ttc	gttcttc	tgt	tttcttag	atggataatt	agggtatcac		300
cagatcccaa	tcaatcttga	tgat	caaagc	aaa	accactt	ttccatgccc	acatggaact		360
tatgcttacc	gtagaatgtc	tttt	gggtta	tgt	aatgcac	cagcttcttt	tcaaagatgc		420
atgatgtctg	tattttctaa	tat	gattgaa	gag	attatgg	aattttcatg	gatgatttct		480
ctgtttatgg	aaaaactttt	gat	agttgtc	ttg	aaaactt	agacagggtt	ttgcaaagat		540
gtgaagaaaa	gtacttagtc	ctta	attgga	aaaa	atgtca	ttttatgggt	aggggaaggaa		600
tagtgctggg	acacctagtg	tct	gaaagag	gtatt	gaggt	cgacaaagct	aaaattgaag		660
taattgaaca	actacctcca	cctt	tgaata	taaa	aggaat	tcgaagcttt	cttggccatg		720
ctgggttttta	tcgtagattc	atta	aggact	ttaca	aaggt	t			761

<210> 131

<211> 254

<212> PRT

<213> Sorghum bicolor

<400> 131

Val	Arg	Lys	Glu	Val	Phe	Lys	Leu	Leu	His	Ala	Glu	Ile	Ile	Tyr	His
1				5					10					15	
Val	Pro	His	Ser	Glu	Trp	Val	Ser	Pro	Val	Gln	Val	Val	Pro	Lys	Lys
			20					25					30		
Gly	Gly	Met	Ile	Val	Val	Thr	Asn	Glu	Lys	Asn	Glu	Leu	Ile	Pro	Gln
		35				40					45				
Arg	Thr	Val	Thr	Gly	Trp	Arg	Met	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn

50		55		60	
Lys Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met					
65		70		75	80
Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Glx					
	85		90		95
Leu Gly Tyr His Gln Ile Pro Ile Asn Leu Asp Asp Gln Ser Lys Thr					
	100		105		110
Thr Phe Pro Cys Pro His Gly Thr Tyr Ala Tyr Arg Arg Met Ser Phe					
	115		120		125
Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Val					
	130		135		140
Phe Ser Asn Met Ile Glu Ile Met Glu Ile Phe Met Asp Asp Phe					
145		150		155	160
Ser Val Tyr Gly Lys Thr Phe Asp Ser Cys Leu Glu Asn Leu Asp Arg					
	165		170		175
Val Leu Gln Arg Cys Glu Glu Lys Tyr Leu Val Leu Asn Trp Lys Lys					
	180		185		190
Cys His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Leu Val Ser					
	195		200		205
Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Glu Val Ile Glu Gln					
	210		215		220
Leu Pro Pro Pro Leu Asn Ile Lys Gly Ile Arg Ser Phe Leu Gly His					
225		230		235	240
Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val					
	245		250		

<210> 132
 <211> 763
 <212> DNA
 <213> Sorghum bicolor

<400> 132					60
gtgcggaag aggtcgtcaa gctctatcat gctgggatta tttatcctgt gccacatagt					120
gagtgggtta gccctgttca agtagtgcca aagaaagaag gaatgacggt cgtaggaat					180
gagaagaatg aactcatccc tcaacaaatt gtcactagat ggcgtatgtg tattgactat					240
cgaaaactca acaaagctac aaagaaagat cactttccgt tacccttcat tgatgaaatg					300
ttggaatggc ttgcaaacca ctctttcttc tgtttccttg atggttattc tggatatcac					360
caaatcccaa tccaccaga tgaccaagaa aagactacct ttacatgccc gtattgaact					420
tatgcatact gacgaatgtc gttcggattg tgcaatgtc tagcttcttt tccagcggtg					480
catgatgtct attttctcgg acatgattga gaagatcatg gaggttttca tggatgattt					540
taccgtctat ggcaaacct tcgatcattg tttggagaat ttagatagag tcttgcagcg					600
atgtgaggaa aatcacttaa tcttgaactg ggagaaatgt cattttatgg ttcaggaagg					660
aatagtgcta ggacataaag tgtccgaacg tggatatagat gtggacaaag caaagattaa					720
agttattgaa aaacttccac ctcacacgaa tgtgaaagga atccatagct ttttgggaca					763
tgcagggttc tatagacgct tcatcaagga tttcacaaag gtt					

<210> 133
 <211> 254
 <212> PRT
 <213> Sorghum bicolor

<400> 133					
Val Arg Lys Glu Val Val Lys Leu Tyr His Ala Gly Ile Ile Tyr Pro					
1	5		10		15
Val Pro His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys					
	20		25		30
Glu Gly Met Thr Val Val Arg Asn Glu Lys Asn Glu Leu Ile Pro Gln					

35					40					45					
Gln	Ile	Val	Thr	Arg	Trp	Arg	Met	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn
50					55					60					
Lys	Ala	Thr	Lys	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Glu	Met
65					70					75					80
Leu	Glu	Trp	Leu	Ala	Asn	His	Ser	Phe	Phe	Cys	Phe	Leu	Asp	Gly	Tyr
				85					90					95	
Ser	Gly	Tyr	His	Gln	Ile	Pro	Ile	His	Pro	Asp	Asp	Gln	Glu	Lys	Thr
			100					105					110		
Thr	Phe	Thr	Cys	Pro	Tyr	Glx	Thr	Tyr	Ala	Tyr	Glx	Arg	Met	Ser	Phe
			115				120					125			
Gly	Leu	Cys	Asn	Ala	Leu	Ala	Ser	Phe	Gln	Arg	Cys	Met	Met	Ser	Ile
130					135					140					
Phe	Ser	Asp	Met	Ile	Glu	Lys	Ile	Met	Glu	Val	Phe	Met	Asp	Asp	Phe
145					150					155					160
Thr	Val	Tyr	Gly	Lys	Thr	Phe	Asp	His	Cys	Leu	Glu	Asn	Leu	Asp	Arg
				165					170					175	
Val	Leu	Gln	Arg	Cys	Glu	Glu	Asn	His	Leu	Ile	Leu	Asn	Trp	Glu	Lys
			180					185					190		
Cys	His	Phe	Met	Val	Gln	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Val	Ser
			195				200					205			
Glu	Arg	Gly	Ile	Asp	Val	Asp	Lys	Ala	Lys	Ile	Lys	Val	Ile	Glu	Lys
210					215					220					
Leu	Pro	Pro	His	Thr	Asn	Val	Lys	Gly	Ile	His	Ser	Phe	Leu	Gly	His
225					230					235					240
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
				245					250						

<210> 134
 <211> 756
 <212> DNA
 <213> Sorghum bicolor

<400> 134
 aaggaggttt tcaagttgct gcatgcaggg attatatatc ttgtgccgca tagtgagtgg 60
 gtaagcccag ttcaagttgt gcctaaaaag ggaggcatga ctattattat gaatgaaaag 120
 aacgagctaa ttccgcaacg caccgttaca gtatggcgga tgtgcataga ctatagaaaa 180
 ctaaacaag ccacgagaga ggatcacttt cctttacctt tcatagatga gatgctagag 240
 tggtagcaa accattcggt cttctgtttc ttagatggat attgagggtta tcatcagatc 300
 ccgatccatc ccgatgatca aagcaaaacc acttttacat gcccatatgg aacttatgct 360
 taccgtagaa tgtcttttgg gttatgtaat gcactagctt cttttcaaag atgcatgatg 420
 tctatatttt ctgatatgat tgaagagatt atggaagttt tcatggatga tttctctggt 480
 tatggaaaaa cttttgatag ttgtcttaaa aacttagaca aggttttgca aagatgtgaa 540
 gaaaagcact tagtccttaa ttgggaaaaa tgtcatttca tggtaggga aggaatagtg 600
 ctgggacact tagtgtctga aagagctatt gaggtagata aagctaaaaa tgaagtaatt 660
 gaacaactac gtccacctgt gaacataaaa ggaatttgaa gctttcttgg ccatgctggt 720
 tttcatcgta gattcataaa agactttaca aaggtt 756

<210> 135
 <211> 252
 <212> PRT
 <213> Sorghum bicolor

<400> 135
 Lys Glu Val Phe Lys Leu Leu His Ala Gly Ile Ile Tyr Leu Val Pro
 1 5 10 15
 His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys Gly Gly

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<210> 136
<211> 762
<212> DNA
<213> Glycine max
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<210> 137
<211> 254
<212> PRT
<213> Glycine max
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<400> 137
Val Arg Lys Glu Val Val Lys Leu Leu Glu Val Gly Leu Ile Tyr Leu

1	5	10	15
Ile Ser Asp	Ser Ala Trp Val Ser	Leu Val Gln Val Ala Pro	Lys Lys
	20	25	30
Cys Gly Met	Thr Val Val Gln Asn Glu Arg Asn Asp	Leu Ile Pro Thr	
	35	40	45
Arg Thr Val	Thr Gly Glx Arg Met Cys Ile Asp Tyr Cys Lys Leu Asn		
	50	55	60
Glu Ala Thr	Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met		
65		70	75
Leu Glu Arg	Leu Ala Gly Gln Ala Tyr Tyr Cys Phe Leu Asp Arg Tyr		
	85	90	95
Ser Gly Tyr	Asn Gln Ile Ala Val Asp Pro Arg Asp Gln Glu Lys Met		
	100	105	110
Ala Phe Thr	Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Ser Phe		
	115	120	125
Arg Leu Cys	Asn Ala Pro Ala Thr Phe Gln Arg Cys Val Leu Ala Ile		
	130	135	140
Phe Ser Asp	Met Val Glu Lys Ser Ile Glu Val Phe Met Asp Glu Phe		
145		150	155
Ser Ile Phe	Gly Pro Leu Phe Asp Ser Cys Leu Arg Asn Leu Glu Met		
	165	170	175
Val Leu Gln	Arg Cys Val Glx Thr Asn Leu Val Leu Asn Glx Glu Lys		
	180	185	190
Cys His Phe	Met Val Arg Glu Gly Ile Val Met Asp His Asn Ile Ser		
	195	200	205
Ala Arg Gly	Ile Glu Val Asp Gln Ala Lys Ile Asp Val Ile Glu Lys		
	210	215	220
Leu Pro Pro	Pro Leu Asn Val Lys Gly Val Arg Ser Phe Leu Gly His		
225		230	235
Ala Gly Phe	Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val		
	245	250	

<210> 138
 <211> 763
 <212> DNA
 <213> Glycine max

<400> 138	
gtgcgtaagg aggtcttttaa gttcttggag gctggggtca tatatcccat ctctaatagc	60
acttaggttaa gccaggtaca ggtggttccc aagaaagggtg gaatgacagt agtacagaat	120
gagaagaatg acttgatacc aacacgaact gtcactagct ggcgaatatg catcgattat	180
cgcaagctga atgaggccac ccggaaggac cacttccctc tacctttcat ggatcagatg	240
ttggagagac ttgcagggca ggcgtattat tgtttcttgg atggatactc gagatataat	300
cagattgcgg tggaccctag agaccaagag aagacgacct tcacatgccc tttttggcgt	360
ctttgcttac agaaggatgc cattcgggtt atgtaatgca ccagccacat ttcagagggtg	420
catgctggcc attttttcag acatggtgga gaaaaatata gaggtattca tggatgactt	480
ttcagttttt gggccctcat ttgacagttg tttgaggaac cttagagatgg tacttttagag	540
gtgcgtagag actaatatag tgctgaactg ggagaagtgt cattttatgg ttcgagaggg	600
catagtccctg agccacaaga tctcagctag agggattgag gttgaccggg caaagataga	660
cgtcataag aagctgccac caccattgaa tattaaaggt gtcagaagtt tcttagggca	720
tgcaggattc tacaggagat tcataaagga ctttacaaag gtt	763

<210> 139
 <211> 254
 <212> PRT
 <213> Glycine max

<400> 139

Val	Arg	Lys	Glu	Val	Phe	Lys	Phe	Leu	Glu	Ala	Gly	Leu	Ile	Tyr	Pro
1				5					10					15	
Ile	Ser	Asn	Ser	Thr	Glx	Val	Ser	Pro	Val	Gln	Val	Val	Pro	Lys	Lys
		20						25					30		
Gly	Gly	Met	Thr	Val	Val	Gln	Asn	Glu	Lys	Asn	Asp	Leu	Ile	Pro	Thr
		35					40					45			
Arg	Thr	Val	Thr	Ser	Trp	Arg	Ile	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn
	50					55				60					
Glu	Ala	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Met	Asp	Gln	Met
65					70					75				80	
Leu	Glu	Arg	Leu	Ala	Gly	Gln	Ala	Tyr	Tyr	Cys	Phe	Leu	Asp	Gly	Tyr
			85					90						95	
Ser	Arg	Tyr	Asn	Gln	Ile	Ala	Val	Asp	Pro	Arg	Asp	Gln	Glu	Lys	Thr
		100						105					110		
Thr	Phe	Thr	Cys	Pro	Phe	Gly	Val	Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe
		115					120					125			
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Leu	Ala	Ile
	130					135					140				
Phe	Ser	Asp	Met	Val	Glu	Lys	Asn	Ile	Glu	Val	Phe	Met	Asp	Asp	Phe
145					150					155					160
Ser	Val	Phe	Gly	Pro	Ser	Phe	Asp	Ser	Cys	Leu	Arg	Asn	Leu	Glu	Met
			165					170					175		
Val	Leu	Glx	Arg	Cys	Val	Glu	Thr	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys
			180					185					190		
Cys	His	Phe	Met	Val	Arg	Glu	Gly	Ile	Val	Leu	Ser	His	Lys	Ile	Ser
	195						200					205			
Ala	Arg	Gly	Ile	Glu	Val	Asp	Arg	Ala	Lys	Ile	Asp	Val	Ile	Glu	Lys
	210					215					220				
Leu	Pro	Pro	Pro	Leu	Asn	Ile	Lys	Gly	Val	Arg	Ser	Phe	Leu	Gly	His
225					230					235				240	
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
			245						250						

<210> 140

<211> 762

<212> DNA

<213> Glycine max

<400> 140

gtgcgcaagg	aggttttgaa	gcttctagag	ggtgggctta	tctaccccat	ctccgacagc	60
gcttgggtaa	gcccagtcct	ggtggtgtcg	aagaaagagg	gcatgacagt	cattcgaaat	120
gaaaagaatg	acctgatacc	aacacgaact	gtcactagtt	ggaaattatg	catcgattac	180
cgcaagctca	acgaagccac	aaggaaagac	catttccctc	tacccttcat	ggatcagatg	240
ttggagagac	ttgcaggaca	cgcttattat	tgcttcttgg	atgcatactt	tgatataat	300
cagattgttg	tagaccccaa	ggatcaggag	aagatggcct	tcacatgccc	ttttggtgtc	360
tttgcctata	gacggattcc	atttgggttg	tgcaatgcac	ctaccacatt	ccaaatgtgc	420
atgttggcca	tttttgcaga	tatagtggag	aaaagcatcg	aagtattcat	ggatgacttt	480
tcagtatttg	tgccctcatt	agaaagtgtg	ttgaagaagt	tggagatggg	actacaaaga	540
tgcgtagaaa	caaacttagt	actaaattgg	gagaagtgtc	acttcatggg	tcgagaaggc	600
atagtcttag	gccataaaat	ttcgaccoga	ggaattgagg	tagaccaaac	aaagattgat	660
gtcattgaaa	agttgccacc	accatcaaat	gttaaaggca	tcaggagctt	cctaggacaa	720
gccaggttct	acagaagatt	catcaaggac	ttcacaaaag	tt		762

<210> 141

<211> 254

<212> PRT

<213> Glycine max

<400> 141

Val	Arg	Lys	Glu	Val	Leu	Lys	Leu	Leu	Glu	Val	Gly	Leu	Ile	Tyr	Pro
1				5					10					15	
Ile	Ser	Asp	Ser	Ala	Trp	Val	Ser	Pro	Val	Leu	Val	Val	Ser	Lys	Lys
			20					25					30		
Glu	Gly	Met	Thr	Val	Ile	Arg	Asn	Glu	Lys	Asn	Asp	Leu	Ile	Pro	Thr
		35					40				45				
Arg	Thr	Val	Thr	Ser	Trp	Lys	Leu	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn
	50					55				60					
Glu	Ala	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Met	Asp	Gln	Met
65					70					75				80	
Leu	Glu	Arg	Leu	Ala	Gly	His	Ala	Tyr	Tyr	Cys	Phe	Leu	Asp	Ala	Tyr
			85					90						95	
Phe	Gly	Tyr	Asn	Gln	Ile	Val	Val	Asp	Pro	Lys	Asp	Gln	Glu	Lys	Met
			100					105					110		
Ala	Phe	Thr	Cys	Pro	Phe	Gly	Val	Phe	Ala	Tyr	Arg	Arg	Ile	Pro	Phe
		115				120						125			
Gly	Leu	Cys	Asn	Ala	Pro	Thr	Thr	Phe	Gln	Met	Cys	Met	Leu	Ala	Ile
	130					135					140				
Phe	Ala	Asp	Ile	Val	Glu	Lys	Ser	Ile	Glu	Val	Phe	Met	Asp	Asp	Phe
145					150					155				160	
Ser	Val	Phe	Val	Pro	Ser	Leu	Glu	Ser	Cys	Leu	Lys	Lys	Leu	Glu	Met
				165					170					175	
Val	Leu	Gln	Arg	Cys	Val	Glu	Thr	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys
			180					185					190		
Cys	His	Phe	Met	Val	Arg	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Ile	Ser
		195				200						205			
Thr	Arg	Gly	Ile	Glu	Val	Asp	Gln	Thr	Lys	Ile	Asp	Val	Ile	Glu	Lys
	210					215					220				
Leu	Pro	Pro	Pro	Ser	Asn	Val	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	Gln
225					230					235				240	
Ala	Arg	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
			245						250						

<210> 142

<211> 762

<212> DNA

<213> Glycine max

<400> 142

gtgcggaagg	aggttatttaa	gttgctagag	gcagggctca	tttaccta	ctcagatagt	60
tcatagggtta	gtcctgttca	tgttgctctg	aaaaaggag	gtatgacagt	gataaagaat	120
gatagagatg	agttaattcc	tacaagaata	gttactggat	ggaggatggg	tattgattac	180
aagaagctaa	atgaagccac	caggaaagac	cattaccgcg	ttcccttcat	ggatcaaata	240
cttgagagac	ttgcagggca	atcttctctac	tattttattag	atggatactc	gggctacaat	300
caaattgcag	tggatcctca	ggaccaagaa	aagacagctt	tcacatgtcc	ttttgggtga	360
tttgcttatc	gccgcatgtc	gttcgggtta	tgtaatgccc	caactacttt	ccagagatgt	420
atgatggcaa	tttttgctga	catggtaaag	aaatgtattg	aagtttttat	ggacgatttc	480
tctgtctttg	gtgcactctt	tgaaaattgc	ctagcaaatt	tagagaaagt	gttacaacgc	540
tatgaagaat	ctaatttggt	gctcaactgg	gaaaaatgtc	actttatggt	tcaagaaggt	600
atcatgctgg	gacacaagat	ttctagaaga	ggaattaagg	tggataaggc	aaagattgag	660
gttattgata	aacttccacc	tctagttaat	gttagaggca	tacgaagttt	tttgggtcat	720
gctagattct	atcgatgatt	tatcaaggac	ttcaccaaag	tt		762

<210> 143

<211> 254
 <212> PRT
 <213> Glycine max

<400> 143

Val	Arg	Lys	Glu	Val	Ile	Lys	Leu	Leu	Glu	Ala	Gly	Leu	Ile	Tyr	Leu
1				5					10					15	
Ile	Ser	Asp	Ser	Ser	Glx	Val	Ser	Pro	Val	His	Val	Ala	Leu	Lys	Lys
		20						25					30		
Gly	Gly	Met	Thr	Val	Ile	Lys	Asn	Asp	Arg	Asp	Glu	Leu	Ile	Pro	Thr
		35					40					45			
Arg	Ile	Val	Thr	Gly	Trp	Arg	Met	Gly	Ile	Asp	Tyr	Lys	Lys	Leu	Asn
	50					55					60				
Glu	Ala	Thr	Arg	Lys	Asp	His	Tyr	Pro	Leu	Pro	Phe	Met	Asp	Gln	Met
65					70					75					80
Leu	Glu	Arg	Leu	Ala	Gly	Gln	Ser	Ser	Tyr	Tyr	Leu	Leu	Asp	Gly	Tyr
				85					90					95	
Ser	Gly	Tyr	Asn	Gln	Ile	Ala	Val	Asp	Pro	Gln	Asp	Gln	Glu	Lys	Thr
			100					105					110		
Ala	Phe	Thr	Cys	Pro	Phe	Gly	Val	Phe	Ala	Tyr	Arg	Arg	Met	Ser	Phe
		115					120					125			
Gly	Leu	Cys	Asn	Ala	Pro	Thr	Thr	Phe	Gln	Arg	Cys	Met	Met	Ala	Ile
	130					135					140				
Phe	Ala	Asp	Met	Val	Lys	Lys	Cys	Ile	Glu	Val	Phe	Met	Asp	Asp	Phe
145					150					155					160
Ser	Val	Phe	Gly	Ala	Ser	Phe	Glu	Asn	Cys	Leu	Ala	Asn	Leu	Glu	Lys
			165					170					175		
Val	Leu	Gln	Arg	Tyr	Glu	Glu	Ser	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys
		180						185					190		
Cys	His	Phe	Met	Val	Gln	Glu	Gly	Ile	Met	Leu	Gly	His	Lys	Ile	Ser
		195					200					205			
Arg	Arg	Gly	Ile	Lys	Val	Asp	Lys	Ala	Lys	Ile	Glu	Val	Ile	Asp	Lys
	210					215					220				
Leu	Pro	Pro	Leu	Val	Asn	Val	Arg	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His
225					230					235					240
Ala	Arg	Phe	Tyr	Arg	Glx	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
				245					250						

<210> 144
 <211> 761
 <212> DNA
 <213> Glycine max

<400> 144

gtgcggaagg	aggtctttaa	gttgctggaa	gcaggcctta	tttatcccat	ttcggatagt	60
gcatgggtta	gccctatgca	agttgtccct	aagaaaggag	gtatgacagt	cattaagaat	120
gataaagatg	agttgatatc	cacaaggacc	gtcaccgggt	ggagaatgtg	cattgactat	180
cgaaagctga	atgatgcacc	cggaaggacc	attatccact	ccctttcatg	ggccatatgc	240
ttgaaagact	tggtgggcaa	tcctattatt	gttttctaga	tggatattat	ggttataatc	300
agattgttgt	agatcccaaa	gatcaagaga	agacagcttt	cacctaccct	tttgggtgat	360
tcgcatatca	gtgcatgcct	tttgggtctat	gcaatgcccc	agctacattt	cagaggtgta	420
tgatggctat	tttttctgat	atgggtggaaa	tatgcattga	agttttcatg	gacgatttct	480
ctattttttg	gccatccttt	gaagggtgct	tatcaaactt	tgaaaaagta	ttaaagagat	540
gtgaagagtc	caatctagtt	ctcaattgga	agaaatgcca	tttcatgggt	caagaaggaa	600
taatgttggg	gcataaaatt	tcagtaagag	ggatagaggt	ggacaaggca	aagattgatg	660
taattgagaa	actacttgct	cccataaatg	tcaagggaat	aagaagcttc	ttaggacatg	720
cagggttcta	caggcgattc	ataaaagact	tcaccaaagt	t		761

<210> 145
 <211> 254
 <212> PRT
 <213> Glycine max

<400> 145
 Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Ala Trp Val Ser Pro Met Gln Val Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Ile Lys Asn Asp Lys Asp Glu Leu Ile Ser Thr
 35 40 45
 Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
 50 55 60
 Asp Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Gly His Met
 65 70 75 80
 Leu Glu Arg Leu Val Gly Gln Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Tyr Gly Tyr Asn Gln Ile Val Val Asp Pro Lys Asp Gln Glu Lys Thr
 100 105 110
 Ala Phe Thr Tyr Pro Phe Gly Val Phe Ala Tyr Gln Cys Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile
 130 135 140
 Phe Ser Asp Met Val Glu Ile Cys Ile Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Ile Phe Gly Pro Ser Phe Glu Gly Cys Leu Ser Asn Leu Glu Lys
 165 170 175
 Val Leu Lys Arg Cys Glu Glu Ser Asn Leu Val Leu Asn Trp Lys Lys
 180 185 190
 Cys His Phe Met Val Gln Glu Gly Ile Met Leu Gly His Lys Ile Ser
 195 200 205
 Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
 210 215 220
 Leu Leu Ala Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 146
 <211> 762
 <212> DNA
 <213> Glycine max

<400> 146
 gtgcgtaagg aggtgggtcaa gttgcttgaa gtaggactaa tttatccaat ctctgatagt 60
 gcttggtgta gttcgaacta ggtgggtgcct aagaaagggtg gtatgacggt gatccacaat 120
 gataagaatg atcttattcc tacacagaca atcattaggt ggcaaagtgtg tattgactat 180
 cacaagttga atgatgtcac caagaaggac cattttcctc tgccattcat ggaccaaagt 240
 ttagagaggt tagctggcca agctttttat tgttttttgg atgggttattc tgggtataac 300
 caaatagcgg tgcattctta agatcaagag aagactacta tcatatgccc atttggtgtc 360
 tttgcttaca gacaaatgtc atttgaactg tgtaatgccc ctaccacctt ctagagattc 420
 atgatggcca tttttgctga ccttgtggag aaatgcatag aggtgttcat gaatgattc 480
 tctattttcg gctcttccct ttatcattgt ttatccaacc tggaattagt gttacaacgg 540
 tgtgcggaaa ccaatttggt gatgaactgg gagaaatgtc atttcatggt ccaagagggg 600
 attgtcttag gccacaagat ctcttccaga ggggttggagg tggacaaggc aaaaattgat 660

gttattgaga agttgcctcc acctatgaat gtgaaaggca tccgaagttt tctcgaatat 720
 gttggatttt ataggaggtt catcaaagac ttcacgaaag tt 762

<210> 147
 <211> 254
 <212> PRT
 <213> Glycine max

<400> 147
 Val Arg Lys Glu Val Val Lys Leu Leu Glu Val Gly Leu Ile Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Ala Trp Val Ser Ser Asn Glx Val Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Ile His Asn Asp Lys Asn Asp Leu Ile Pro Thr
 35 40 45
 Gln Thr Ile Ile Arg Trp Gln Met Cys Ile Asp Tyr His Lys Leu Asn
 50 55 60
 Asp Val Thr Lys Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ala Gly Gln Ala Phe Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Ala Val His Leu Lys Asp Gln Glu Lys Thr
 100 105 110
 Thr Ile Ile Cys Pro Phe Gly Val Phe Ala Tyr Arg Gln Met Ser Phe
 115 120 125
 Glu Leu Cys Asn Ala Pro Thr Thr Phe Glx Arg Phe Met Met Ala Ile
 130 135 140
 Phe Ala Asp Leu Val Glu Lys Cys Ile Glu Val Phe Met Asn Asp Phe
 145 150 155 160
 Ser Ile Phe Gly Ser Ser Phe Tyr His Cys Leu Ser Asn Leu Glu Leu
 165 170 175
 Val Leu Gln Arg Cys Ala Glu Thr Asn Leu Leu Met Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
 195 200 205
 Ser Arg Gly Leu Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
 210 215 220
 Leu Pro Pro Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Glu Tyr
 225 230 235 240
 Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 148
 <211> 762
 <212> DNA
 <213> Glycine max

<400> 148
 gtgcgtaagg aggttctcaa gcttttggag gttgggctca tatacctcat ctctgacagc 60
 gcttgggttaa gcctagtaca ggtggctccc aagaaatgcg gaatgacagt ggtacaaaat 120
 gagaggaatg acttgatacc aacacgaact gtcactggct agcggatgtg tatcgactac 180
 tgcaagttag atgaagccac acggaaggac catttccct tacctttcat ggatcagatg 240
 ctggagaggc ttgcagggca ggcatactac tgtttcttgg atagatatc aggatacaac 300
 caaatcgcg tagaccccag agatcaggag aagatggcct ttacatgcc ctttggcgtc 360
 tttgcttaca gaaggatgtc attcaggtta tgtaacgcac cagccacatt tcagaggtgc 420
 atgctggcca ttttttcaga catggtggag aagagcatcg aggtatttat ggatgaattc 480
 tcgatttttg gacccttatt tgacagttgc ttaaggaact tagagatggt actacagagg 540

tgcgatataga	ctaacttgggt	actaaattag	gaaaaatgtc	atttcatgggt	tcgagagggga	600
atagtgatgg	gccacaatat	ctcagctaga	gggattgagg	ttgatcagac	aaagatagac	660
gtcattgaga	agttgccacc	accactgaat	gttaaaggcg	tcagaagttt	cttagggcat	720
gcaggtttct	acaggagggtt	cataaaagac	ttcacaaagg	tt		762

<210> 149
 <211> 254
 <212> PRT
 <213> Glycine max

<400> 149

Val	Arg	Lys	Glu	Val	Leu	Lys	Leu	Leu	Glu	Val	Gly	Leu	Ile	Tyr	Leu
1				5					10					15	
Ile	Ser	Asp	Ser	Ala	Trp	Val	Ser	Leu	Val	Gln	Val	Ala	Pro	Lys	Lys
			20					25					30		
Cys	Gly	Met	Thr	Val	Val	Gln	Asn	Glu	Arg	Asn	Asp	Leu	Ile	Pro	Thr
		35					40					45			
Arg	Thr	Val	Thr	Gly	Glx	Arg	Met	Cys	Ile	Asp	Tyr	Cys	Lys	Leu	Asn
	50					55					60				
Glu	Ala	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Met	Asp	Gln	Met
65					70					75				80	
Leu	Glu	Arg	Leu	Ala	Gly	Gln	Ala	Tyr	Tyr	Cys	Phe	Leu	Asp	Arg	Tyr
				85					90					95	
Ser	Gly	Tyr	Asn	Gln	Ile	Ala	Val	Asp	Pro	Arg	Asp	Gln	Glu	Lys	Met
			100					105				110			
Ala	Phe	Thr	Cys	Pro	Phe	Gly	Val	Phe	Ala	Tyr	Arg	Arg	Met	Ser	Phe
	115					120						125			
Arg	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Leu	Ala	Ile
	130					135					140				
Phe	Ser	Asp	Met	Val	Glu	Lys	Ser	Ile	Glu	Val	Phe	Met	Asp	Glu	Phe
145					150					155				160	
Ser	Ile	Phe	Gly	Pro	Leu	Phe	Asp	Ser	Cys	Leu	Arg	Asn	Leu	Glu	Met
			165					170					175		
Val	Leu	Gln	Arg	Cys	Val	Glx	Thr	Asn	Leu	Val	Leu	Asn	Glx	Glu	Lys
		180						185					190		
Cys	His	Phe	Met	Val	Arg	Glu	Gly	Ile	Val	Met	Gly	His	Asn	Ile	Ser
	195						200					205			
Ala	Arg	Gly	Ile	Glu	Val	Asp	Gln	Thr	Lys	Ile	Asp	Val	Ile	Glu	Lys
	210					215					220				
Leu	Pro	Pro	Pro	Leu	Asn	Val	Lys	Gly	Val	Arg	Ser	Phe	Leu	Gly	His
225					230					235				240	
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
				245					250						

<210> 150
 <211> 761
 <212> DNA
 <213> Glycine max

<400> 150

gtgcgtaagg	agggtttttaa	gttgctggaa	gcagggtctta	tttatcccat	ttcggatagt	60
gcatgggtta	gccctgtgca	ggttggtccc	aagaaagaag	gtaagacagt	cattaaggat	120
gaaaaggatg	agttgatatc	cacaaggact	atcaccgggt	ggagaatgtg	cattgactat	180
cagaagctga	atgatgccac	ccggaaggac	cattatccac	tccttttcat	ggaccaaag	240
cttgaaagac	ttgccgggca	atcttattat	tgttttctgg	atggatatcc	tggttataat	300
cagattgatg	tagatcccaa	ggatcaagag	aagactgctt	tcacctaccc	ttttggtgta	360
ttcgccctatc	ggcgcatgcc	ctttggtttg	tgcaatgccc	cagctacatt	tcagaggtgt	420

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atgatgacta ttttttctga tatggtggaa aaatgaattg aagttttcat ggacgatttc 480
tctatttttg ggccatcttt tgaagggtgc ttatcaaadc ttgaaagagt attaaagaga 540
cgtgaagagt ccaaactagt tctcaattgg gagaaatgcc atttcatggg tcaagaagga 600
atagtgtggg gcataaaaatt tcagtaagag ggatagaggt ggacaaggca aagattgatg 660
taatagagaa actacctcct cccatgaatg tcaagggaat aagaagcttc ctaggacatg 720
caggggttcta caagcgattc atcaaagatt tcacaaaggt t 761

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<210> 151

<211> 254

<212> PRT

<213> Glycine max

<400> 151

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Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro
1          5          10          15
Ile Ser Asp Ser Ala Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
20          25          30
Glu Gly Lys Thr Val Ile Lys Asp Glu Lys Asp Glu Leu Ile Ser Thr
35          40          45
Arg Thr Ile Thr Gly Trp Arg Met Cys Ile Asp Tyr Gln Lys Leu Asn
50          55          60
Asp Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Asp Gln Met
65          70          75          80
Leu Glu Arg Leu Ala Gly Gln Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr
85          90          95
Ser Gly Tyr Asn Gln Ile Asp Val Asp Pro Lys Asp Gln Glu Lys Thr
100         105         110
Ala Phe Thr Tyr Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe
115         120         125
Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Thr Ile
130         135         140
Phe Ser Asp Met Val Glu Lys Glx Ile Glu Val Phe Met Asp Asp Phe
145         150         155         160
Ser Ile Phe Gly Pro Ser Phe Glu Gly Cys Leu Ser Asn Leu Glu Arg
165         170         175
Val Leu Lys Arg Arg Glu Glu Ser Lys Leu Val Leu Asn Trp Glu Lys
180         185         190
Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
195         200         205
Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
210         215         220
Leu Pro Pro Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
225         230         235         240
Ala Gly Phe Tyr Lys Arg Phe Ile Lys Asp Phe Thr Lys Val
245         250

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<210> 152

<211> 762

<212> DNA

<213> Glycine max

<400> 152

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gtgcggaag aggtattcaa gttactagag gcagggtc tctacccaat ttcagatagc 60
tcctgggtta gtccggttca agttgttcca aaaaaaggag ggatgacagt ggtaaaaaat 120
gatagaaatg agctaattcc tacaagaaga gtcaccagat ggagaatgtg tattgattat 180
aggaagctca atgaagccac aagaaaagac cattacccac ttcccttcat ggatcaaatg 240
cttaagagac ttgcaaggca atccttctac cgtttcttgg acggatactc aggttacaat 300

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cagattgcag tggatcctca ggatcaagaa aaaacagctt ttacatgtcc tttcagtgtt 360
tttgcttata gccgcatgcc gttcgggtta tgtaatgcct ctactacttt tcagagatgt 420
atgatggcaa tttttgatga catggttagag aaatgtattg aagtctttat ggatgatttt 480
tcgttctttg gtgcatcttt tggaaattgc ttagcaaatt tagagaaagt gttacaacgt 540
tgtgaaaaat ctaatttggt gcttaactgg gaaaaatgtc actttatggt acaagaaggt 600
attgtgctag gacacaaaat ctctaaaaga ggaattgagg tggttaaaaga aaaactagat 660
gttattgata aacttccacc cccagttaat gtaaaaggca tacacagttt tttgggtcat 720
gttgattttt atcggcgatt cataaaggac ttcaccaaag tt 762

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<210> 153
 <211> 254
 <212> PRT
 <213> Glycine max

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<400> 153
Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro
1          5          10          15
Ile Ser Asp Ser Ser Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
20          25          30
Gly Gly Met Thr Val Val Lys Asn Asp Arg Asn Glu Leu Ile Pro Thr
35          40          45
Arg Arg Val Thr Arg Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
50          55          60
Glu Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Asp Gln Met
65          70          75          80
Leu Lys Arg Leu Ala Arg Gln Ser Phe Tyr Arg Phe Leu Asp Gly Tyr
85          90          95
Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Gln Asp Gln Glu Lys Thr
100          105          110
Ala Phe Thr Cys Pro Phe Ser Val Phe Ala Tyr Arg Arg Met Pro Phe
115          120          125
Gly Leu Cys Asn Ala Ser Thr Thr Phe Gln Arg Cys Met Met Ala Ile
130          135          140
Phe Asp Asp Met Val Glu Lys Cys Ile Glu Val Phe Met Asp Asp Phe
145          150          155          160
Ser Phe Phe Gly Ala Ser Phe Gly Asn Cys Leu Ala Asn Leu Glu Lys
165          170          175
Val Leu Gln Arg Cys Glu Lys Ser Asn Leu Val Leu Asn Trp Glu Lys
180          185          190
Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
195          200          205
Lys Arg Gly Ile Glu Val Val Lys Glu Lys Leu Asp Val Ile Asp Lys
210          215          220
Leu Pro Pro Pro Val Asn Val Lys Gly Ile His Ser Phe Leu Gly His
225          230          235          240
Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
245          250

```

<210> 154
 <211> 761
 <212> DNA
 <213> Glycine max

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<400> 154
gtgcgtaaaag aagtttttgaa gctgctagaa gcagacctta tttatcccat ttcggatagt 60
acatgggtta gccctgtgca agttgtcccc gagaaaggag gtatgacagt cattaagaat 120
gataaagatg agttgatatc cacaaggact gtcaccgggt gagaatgtgc attgactatc 180

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ggaagctgaa tgatgccacc cagaaggacc attattcact cccctttcatg gaccagatgc 240
ttgaaagact tgccggacaa tcctattatt gttttctgaa tggatactct ggctataatc 300
agattgtggt agatcccaaa gatcaggaga aaactgcttt cacctgcctt tttgggtgat 360
ttgcatacaa gcgtatgcat tttggcttgt gtaatgctcc aactacgtgt cagaggtgta 420
tgatgactat tttttctggt atcgtggaaa aatgcattga acttttcatg gacgatttct 480
ctatTTTTTgg gccatctttt gaaggctact tatcaaacct tgaaagagta ttacagagat 540
gtgaagagtc taatctagtt ctcaattggg agaaatgcc aattcatgggt caagaaggaa 600
tagtgctggg gcataaaatt tcagtaagag ggatagaggt ggacaaggca aagattgatg 660
taattgagaa actacctcct cccatgattg tcaagggaat aagaagcctc ctaggacatg 720
tagggttcta caggcgattc atcaaagact tcacaaaggt t 761

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<210> 155

<211> 254

<212> PRT

<213> Glycine max

<400> 155

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Val Arg Lys Glu Val Leu Lys Leu Leu Glu Ala Asp Leu Ile Tyr Pro
 1           5           10           15
Ile Ser Asp Ser Thr Trp Val Ser Pro Val Gln Val Val Pro Glu Lys
          20           25           30
Gly Gly Met Thr Val Ile Lys Asn Asp Lys Asp Glu Leu Ile Ser Thr
          35           40           45
Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
          50           55           60
Asp Ala Thr Gln Lys Asp His Tyr Ser Leu Pro Phe Met Asp Gln Met
65           70           75           80
Leu Glu Arg Leu Ala Gly Gln Ser Tyr Tyr Cys Phe Leu Asn Gly Tyr
          85           90           95
Ser Gly Tyr Asn Gln Ile Val Val Asp Pro Lys Asp Gln Glu Lys Thr
          100          105          110
Ala Phe Thr Cys Leu Phe Gly Val Phe Ala Tyr Lys Arg Met His Phe
          115          120          125
Gly Leu Cys Asn Ala Pro Thr Thr Cys Gln Arg Cys Met Met Thr Ile
          130          135          140
Phe Ser Gly Ile Val Glu Lys Cys Ile Glu Leu Phe Met Asp Asp Phe
145          150          155          160
Ser Ile Phe Gly Pro Ser Phe Glu Gly Tyr Leu Ser Asn Leu Glu Arg
          165          170          175
Val Leu Gln Arg Cys Glu Glu Ser Asn Leu Val Leu Asn Trp Glu Lys
          180          185          190
Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
          195          200          205
Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
          210          215          220
Leu Pro Pro Pro Met Ile Val Lys Gly Ile Arg Ser Leu Leu Gly His
225          230          235          240
Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
          245          250

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<210> 156

<211> 762

<212> DNA

<213> Glycine max

<400> 156

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gtgcgtaagg aggttttttaa gttgctggaa gcaggctctta tttatcccat ttcggatagt

```

60

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gcattgggtta gccctgtgca ggttgtcccc aagaaagaag gtaagacagt cattaaggat 120
gaaaaagatg agttgatatc cacaaggact atcacgggtt ggagaatgtg cattgactat 180
cagaagctga atgatgccac ccggaaggac cattatccac tccctttcat ggaccaaagt 240
cttgaaagac ttgccgggca atcttattat tgttttctgg atggatattc tggttataat 300
cagattgatg tagatcccaa ggatcaagag aagactgctt tcacctacc ttttgggtga 360
ttcgccctatc ggccgatgcc ctttgggttg tgcaatgccc cagctacatt tcagaggtgt 420
atgatgacta ttttttctga tatggtggaa aaatgaattg aagttttcat ggacgatgtc 480
tctatttttg ggccatcttt tgaagggtgc ttatcaaadc ttgaaagagt attaaagaga 540
cgtgaagagt ccaaactagt tctcaattgg gagaaatgcc atttcatggt tcaagaagga 600
atagtgttgg ggcataaaat ttcagtaaga gggatagagg tggacaaggc aaagattgat 660
gtaatagaga aactacctcc tcccatgaat gtcaagggaa taagaagctt cctaggacat 720
gcagggttct acaagcgatt catcaaagac ttctcaaaag tt 762

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<210> 157
 <211> 254
 <212> PRT
 <213> Glycine max

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<400> 157
Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro
 1           5           10           15
Ile Ser Asp Ser Ala Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
      20           25           30
Glu Gly Lys Thr Val Ile Lys Asp Glu Lys Asp Glu Leu Ile Ser Thr
      35           40           45
Arg Thr Ile Thr Gly Trp Arg Met Cys Ile Asp Tyr Gln Lys Leu Asn
      50           55           60
Asp Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Asp Gln Met
      65           70           75           80
Leu Glu Arg Leu Ala Gly Gln Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr
      85           90           95
Ser Gly Tyr Asn Gln Ile Asp Val Asp Pro Lys Asp Gln Glu Lys Thr
      100          105          110
Ala Phe Thr Tyr Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe
      115          120          125
Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Thr Ile
      130          135          140
Phe Ser Asp Met Val Glu Lys Glx Ile Glu Val Phe Met Asp Asp Val
      145          150          155          160
Ser Ile Phe Gly Pro Ser Phe Glu Gly Cys Leu Ser Asn Leu Glu Arg
      165          170          175
Val Leu Lys Arg Arg Glu Glu Ser Lys Leu Val Leu Asn Trp Glu Lys
      180          185          190
Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
      195          200          205
Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
      210          215          220
Leu Pro Pro Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
      225          230          235          240
Ala Gly Phe Tyr Lys Arg Phe Ile Lys Asp Phe Ser Lys Val
      245          250

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<210> 158
 <211> 761
 <212> DNA
 <213> Glycine max

<400> 158

gtg	cggaagg	aggttcttaa	gctcctggaa	gcagggctca	tctatcttat	ctcagatagt	60
gttgggtgag	tccagtgc	gtgggtccca	agaaggggtg	gaagactgtg	gtgagaaatg		120
agaaaaatga	cctcattcta	acccgaactg	tcacaggatg	gagaatgtgc	atagattatc		180
ggaagttgaa	tgatgccatc	aagaaggatc	acttccctct	accattcata	gatcagatgc		240
ttgagaggtt	agcaagccag	tctttctatt	atttcttgga	tgaatattct	agatacaatc		300
agattgctat	acatcccaag	gaccaagaga	agattgcatt	tacatgcca	tttgggtgtct		360
ttgcctatag	aaggatgcca	tttgaactat	gcaatgctcc	agctaccttt	tagaggcata		420
tgctagccat	attcgctaac	atgggtggaga	aatgcatcga	agtgttcata	gatgattttt		480
cgggtgtttg	tccatccttt	gtttgttggt	tgaccaattt	agagctagt	ttgaagtact		540
gtgaggagac	aaatttagta	ttgaattggg	agaaatgtca	tttcatggtc	caagaaggaa		600
ttatgttggg	gcataaaatt	tttgctagag	gtattgaggt	ggacaaggcc	aaaattgatg		660
ttattgaaaa	gctgcctcca	ccagtcaatg	taaaaggcat	caggagtttt	cttggacaca		720
ctggtttctt	caggcgtttc	atcaaggact	tcacaaaagt	t			761

<210> 159

<211> 254

<212> PRT

<213> Glycine max

<400> 159

Val	Arg	Lys	Glu	Val	Leu	Lys	Leu	Leu	Glu	Ala	Gly	Leu	Ile	Tyr	Leu	
1				5					10					15		
Ile	Ser	Asp	Ser	Ala	Trp	Val	Ser	Pro	Val	His	Val	Val	Pro	Lys	Lys	
			20					25					30			
Gly	Gly	Lys	Thr	Val	Val	Arg	Asn	Glu	Lys	Asn	Asp	Leu	Ile	Leu	Thr	
		35					40				45					
Arg	Thr	Val	Thr	Gly	Trp	Arg	Met	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn	
	50					55				60						
Asp	Ala	Ile	Lys	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met	
65					70				75					80		
Leu	Glu	Arg	Leu	Ala	Ser	Gln	Ser	Phe	Tyr	Tyr	Phe	Leu	Asp	Glu	Tyr	
			85						90				95			
Ser	Arg	Tyr	Asn	Gln	Ile	Ala	Ile	His	Pro	Lys	Asp	Gln	Glu	Lys	Ile	
			100					105					110			
Ala	Phe	Thr	Cys	Pro	Phe	Gly	Val	Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe	
		115					120					125				
Glu	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Glx	Arg	His	Met	Leu	Ala	Ile	
	130					135				140						
Phe	Ala	Asn	Met	Val	Glu	Lys	Cys	Ile	Glu	Val	Phe	Ile	Asp	Asp	Phe	
145					150				155					160		
Ser	Val	Phe	Gly	Pro	Ser	Phe	Val	Cys	Cys	Leu	Thr	Asn	Leu	Glu	Leu	
			165					170					175			
Val	Leu	Lys	Tyr	Cys	Glu	Glu	Thr	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys	
			180					185					190			
Cys	His	Phe	Met	Val	Gln	Glu	Gly	Ile	Met	Leu	Gly	His	Lys	Ile	Phe	
	195						200					205				
Ala	Arg	Gly	Ile	Glu	Val	Asp	Lys	Ala	Lys	Ile	Asp	Val	Ile	Glu	Lys	
	210					215					220					
Leu	Pro	Pro	Pro	Val	Asn	Val	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His	
225					230				235					240		
Thr	Gly	Phe	Phe	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val			
			245					250								

<210> 160

<211> 762

<212> DNA

<213> Pisum sativum

<400> 160

gtg	cgcaagg	aagtactcaa	gttg	tttagat	tcgggaatga	ttt	accccat	ttctgacagc	60
tcgtgggtaa	gtccagtgca	cgtgg	tacca	aagaaaggag	gaacctcagt	aatt	tttaa	at	120
gaaaagaatg	aactgatccc	aactcgcaca	gtgacagggt	ggcgagtatg	catcgatcac				180
agaagactga	acacagcaac	aagaaaggat	cattttcctc	tcccttttat	tgatcaa	atg			240
ttagaaagac	ttgcagggtca	tgagtattat	tgctttctgg	atggatattc	gggatacaat				300
caaattgttg	tagccccgga	agatcaggaa	aaaactgcat	ttacatgtcc	ttatggtatt				360
ttcgtttaca	gacggatgcc	atttgggcta	tgcaatgccc	cagctacttt	tcagagggtgt				420
atgacatcta	tattctccga	catgcttgaa	aagtatatga	aggtgtttat	ggatgatttc				480
tctgtgtttg	gttcttcttt	tgataattgt	ttagctaact	tgtctcttgt	tttgcaaaga				540
tgtcaggaaa	ctaaccttgt	tctcaattgg	gagaaatgtc	atttcatggt	gcaggaagga				600
attgtgctag	gacacaaaat	ttcccacaaa	ggaattgaag	tggacaaaagc	caaagtggag				660
gttatagcta	acctcccacc	tccggtgaat	gaaaaaggga	taaggagttt	tttgggtcat				720
gcagggtttt	atcgcagggt	catcaaagac	ttcaciaaag	tt					762

<210> 161

<211> 254

<212> PRT

<213> Pisum sativum

<400> 161

Val	Arg	Lys	Glu	Val	Leu	Lys	Leu	Leu	Asp	Ser	Gly	Met	Ile	Tyr	Pro	
1				5					10						15	
Ile	Ser	Asp	Ser	Ser	Trp	Val	Ser	Pro	Val	His	Val	Val	Pro	Lys	Lys	
			20					25					30			
Gly	Gly	Thr	Ser	Val	Ile	Leu	Asn	Glu	Lys	Asn	Glu	Leu	Ile	Pro	Thr	
		35					40					45				
Arg	Thr	Val	Thr	Gly	Trp	Arg	Val	Cys	Ile	Asp	His	Arg	Arg	Leu	Asn	
	50					55					60					
Thr	Ala	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met	
65					70					75					80	
Leu	Glu	Arg	Leu	Ala	Gly	His	Glu	Tyr	Tyr	Cys	Phe	Leu	Asp	Gly	Tyr	
			85					90						95		
Ser	Gly	Tyr	Asn	Gln	Ile	Val	Val	Ala	Pro	Glu	Asp	Gln	Glu	Lys	Thr	
			100					105					110			
Ala	Phe	Thr	Cys	Pro	Tyr	Gly	Ile	Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe	
		115					120					125				
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Thr	Ser	Ile	
	130					135					140					
Phe	Ser	Asp	Met	Leu	Glu	Lys	Tyr	Met	Lys	Val	Phe	Met	Asp	Asp	Phe	
145				150						155					160	
Ser	Val	Phe	Gly	Ser	Ser	Phe	Asp	Asn	Cys	Leu	Ala	Asn	Leu	Ser	Leu	
			165					170					175			
Val	Leu	Gln	Arg	Cys	Gln	Glu	Thr	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys	
		180						185					190			
Cys	His	Phe	Met	Val	Gln	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Ile	Ser	
	195						200					205				
His	Lys	Gly	Ile	Glu	Val	Asp	Lys	Ala	Lys	Val	Glu	Val	Ile	Ala	Asn	
	210				215						220					
Leu	Pro	Pro	Pro	Val	Asn	Glu	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His	
225				230						235					240	
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val			
			245					250								

<210> 162

<211> 762
 <212> DNA
 <213> Pisum sativum

<400> 162
 gtgCGtaagg aggtctttaa actattggat gcgggaatga tttacccgat ctCGgatagt 60
 ccgtgggtta gtcccgTGca cgtgggtccg aagaagggtg gaatgaccgt aatccgtaat 120
 gacaaagacg aattgatccc gactaaagt gcaacggggt ggagaatatg tatagattat 180
 agacagttga ataccgcgac tcgaaaggac cattttccac tcccatttat ggatcaaatg 240
 cttgaaagac tatcggggcca acaatactat tgtttcttgg acggctactc cgggtacaac 300
 caaattgcgg ttgaccCGgt tgatcatgag aagacggctt tcacgtgtcc gtttggagtg 360
 ttCGcataca gaaaaatgcc ctttgggctg tgcaatgcac cggcgacttt ccaacgatgc 420
 gtCctagcca tttttgCCga tctaatagag aaaacaatgg acgtcttcat ggatgacttc 480
 tcgggtatttg gtgggacggt tagtctatgc ttggcaaatt tgaagacggt gttggaaagg 540
 tgtgtgaaga ccaatttggg gctaaattgg gaaaagtgtc acttcatggt gaccgagggg 600
 atcgtgctag gccacaaagt ctctaaaagg gggcttgaag tggatagagc taaggttgaa 660
 gtaattgaaa aattaccccc tccggtgaat gtgaaaggca tccgtagctt tttggggcac 720
 gcgggggttt accggcgctt cattaaagac ttctcaaaa tt 762

<210> 163
 <211> 254
 <212> PRT
 <213> Pisum sativum

<400> 163
 Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Met Ile Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Pro Trp Val Ser Pro Val His Val Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Ile Arg Asn Asp Lys Asp Glu Leu Ile Pro Thr
 35 40 45
 Lys Val Ala Thr Gly Trp Arg Ile Cys Ile Asp Tyr Arg Gln Leu Asn
 50 55 60
 Thr Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ser Gly Gln Gln Tyr Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Val Asp His Glu Lys Thr
 100 105 110
 Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Lys Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Val Leu Ala Ile
 130 135 140
 Phe Ala Asp Leu Ile Glu Lys Thr Met Asp Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Phe Gly Gly Thr Phe Ser Leu Cys Leu Ala Asn Leu Lys Thr
 165 170 175
 Val Leu Glu Arg Cys Val Lys Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Thr Glu Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205
 Lys Arg Gly Leu Glu Val Asp Arg Ala Lys Val Glu Val Ile Glu Lys
 210 215 220
 Leu Pro Pro Pro Val Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Ser Lys Val
 245 250

<210> 164
 <211> 762
 <212> DNA
 <213> Pisum sativum

<400> 164
 gtgcggaagg aggtctttaa attgttggat gcggggatga tttacccgat ctcggatagt 60
 ccatgggtta gtcctgtgca cgttgttccg aagaaggggg ggattaccgt aatccggaat 120
 gacaaggatg aattgatccc cactaaagtt gaaacggggg ggagaatgtg tattgattat 180
 aggcggttga ataccgcgac tcgaaaagac cattttccac tcccatttat ggatcaaata 240
 ctcgaaagac tatcggggcca acaatattat tgttttttgg acggctactc cgggtacaac 300
 caaattgcgg ttgacccggc cgatcatgag aagacggctt tcacatgtcc gtttggagtg 360
 ttgcataacc gaaaaatgcc ctttgggctg tgcaatgcac cggcgacctt ccaacgatgt 420
 gtccaagcca tttttgtcga tctgatagag aaaacaatgg aagtcttcat ggatgacttc 480
 tcggtatttg gtgggtcttt tagtctatgc ttggcgaaact tgaaaacggg gttggagaga 540
 tgtgtgaaga ccaatttggt gcttaattgg gagaagtgtc acttcatggg gaccgagggg 600
 atcgtgctag gccacaaagt ctctagaagg gggcttgaag tggatagagc taagggtgaa 660
 gtgatagaaa aattacctcc tccggtgaat gtgaagggca tccgaagctt tttggggcac 720
 gccgggttct accggcgctt cattaaagat ttcacaaagg tt 762

<210> 165
 <211> 254
 <212> PRT
 <213> Pisum sativum

<400> 165
 Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Met Ile Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Pro Trp Val Ser Pro Val His Val Val Pro Lys Lys
 20 25 30
 Gly Gly Ile Thr Val Ile Arg Asn Asp Lys Asp Glu Leu Ile Pro Thr
 35 40 45
 Lys Val Glu Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Arg Leu Asn
 50 55 60
 Thr Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ser Gly Gln Gln Tyr Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Ala Asp His Glu Lys Thr
 100 105 110
 Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Lys Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Val Gln Ala Ile
 130 135 140
 Phe Val Asp Leu Ile Glu Lys Thr Met Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Phe Gly Gly Ser Phe Ser Leu Cys Leu Ala Asn Leu Lys Thr
 165 170 175
 Val Leu Glu Arg Cys Val Lys Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Thr Glu Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205
 Arg Arg Gly Leu Glu Val Asp Arg Ala Lys Val Glu Val Ile Glu Lys
 210 215 220
 Leu Pro Pro Pro Val Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 166
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated oligonucleotide

<221> misc_feature
 <222> 6, 15, 16, 18
 <223> n = A,T,C or G

<400> 166
 gtgcgnaarg argtnntnaa ryt

23

<210> 167
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> plant retroelement sequence

<400> 167
 Val Arg Lys Glu Val Leu Lys Leu
 1 5

<210> 168
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated oligonucleotide

<221> misc_feature
 <222> 7
 <223> n = A,T,C or G

<400> 168
 aacyttngwr aartcyttta traa

24

<210> 169
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> plant retroelement sequence

<400> 169
 Val Lys Ser Phe Asp Lys Ile Phe
 1 5

<210> 170
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 170
 gggatccgca attagaatct 20

<210> 171
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 171
 cgaattcggg ccacttcgga 20

<210> 172
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 172
 ccacaagatt ctaattgcgg attc 24

<210> 173
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 173
 ccgaaatgga ccgaacccga catc 24

<210> 174
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 174
 tttccaggct cttgacgaga ttg 24

<210> 175
 <211> 22

<212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 175
 cgactcgagc tccatagcga tg 22

<210> 176
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 176
 cggattgggc cgaaatggac cgaa 24

<210> 177
 <211> 18
 <212> DNA
 <213> Arabidopsis thaliana

<400> 177
 gaggacttgg ggggcaaa 18

<210> 178
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> exemplary motif

<221> VARIANT
 <222> 2-3, 5-7, 9-12
 <223> Xaa = Any Amino Acid

<400> 178
 Cys Xaa Xaa Cys Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Cys
 1 5 10

<210> 179
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> exemplary motif

<400> 179
 Leu Ile Asp Leu Gly Ala
 1 5

<210> 180

<211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<400> 180
 Lys Thr Ala Phe
 1

<210> 181
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<221> VARIANT
 <222> 2
 <223> Xaa = Pro or Ser

<400> 181
 Met Xaa Phe Gly Leu Cys Asn Ala
 1 5

<210> 182
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<221> VARIANT
 <222> 1
 <223> Xaa = Val, Ile, or Met

<221> VARIANT
 <222> 9
 <223> Xaa = Ser or Trp

<221> VARIANT
 <222> 10
 <223> Xaa = Val or Ile

<400> 182
 Xaa Glu Val Phe Met Asp Asp Phe Xaa Xaa
 1 5 10

<210> 183
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> 12

<223> Xaa = Ile or Val

<400> 183

Phe	Glu	Leu	Met	Cys	Asp	Ala	Ser	Asp	Tyr	Ala	Xaa	Gly	Ala	Val	Leu
1				5					10					15	
Gly	Gln	Arg													

<210> 184

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> 4

<223> Xaa = Thr or Ile

<221> VARIANT

<222> 8

<223> Xaa = Leu or Met

<221> VARIANT

<222> 13

<223> Xaa = Phe or Tyr

<221> VARIANT

<222> 15

<223> Xaa = Leu or Phe

<221> VARIANT

<222> 19

<223> Xaa = Arg or Lys

<221> VARIANT

<222> 23

<223> Xaa = Ile or Val

<221> VARIANT

<222> 26

<223> Xaa = Arg or Lys

<400> 184

Tyr	Ala	Thr	Xaa	Glu	Lys	Glu	Xaa	Leu	Ala	Ile	Val	Xaa	Ala	Xaa	Glu
1				5					10					15	
Lys	Phe	Xaa	Ser	Tyr	Leu	Xaa	Gly	Ser	Xaa	Val					
			20					25							

<210> 185

<211> 46

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> 4, 6-7, 11-40, 43

<223> Xaa = Any Amino Acid

<400> 185

His	Cys	His	Xaa	Ser	Xaa	Xaa	Gly	Gly	His	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10					15	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25						30	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Asp	Xaa	Cys	Gln	Arg		
			35				40						45		

<210> 186

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> 6

<223> Xaa = Ile, Val, or Met

<400> 186

Trp	Gly	Ile	Asp	Phe	Xaa	Gly	Pro
1				5			

<210> 187

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> 7

<223> Xaa = Any Amino Acid

<221> VARIANT

<222> 10

<223> Xaa = Ala or Val

<400> 187

Pro	Tyr	His	Pro	Gln	Thr	Xaa	Gly	Gln	Xaa	Glu
1				5					10	

<210> 188

<211> 13

<212> DNA

<213> Artificial Sequence

<220>
 <223> consensus sequence

<221> misc_feature
 <222> 11, 12
 <223> n = A,T,C or G

<400> 188
 atttgggggra nnt

13

<210> 189
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<221> VARIANT
 <222> 5, 8
 <223> Xaa = Arg or Lys

<400> 189
 Gln Met Ala Ser Xaa Lys Arg Xaa Ala
 1 5

<210> 190
 <211> 6
 <212> PRT
 <213> Pisum sativum

<400> 190
 Ala Ser Lys Lys Arg Lys
 1 5

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 Genew